

Method for HLA typing

The present invention relates to a method for HLA typing by the unambiguous determination of short DNA sequence elements (2-6 bases) at a given position 5 simultaneously on both parental alleles at a selected number of positions in HLA genes, comprised of the steps for each position of a) hybridising a combination of oligonucleotides (primers) complementary to all known sequence variants to a DNA strand upstream of a given position; b) carrying out a primer extension reaction with at least one of the four dNTP substrates substituted by a terminating analog; c) 10 analysing the products by mass spectrometry, with the resulting masses allowing unambiguous identification of the used primers and the added bases. This method is particularly well suited for DNA-based HLA typing and in combination with a suitable selection of sites tested, it is superior in ease of operation to conventional HLA typing methods.

15 The most important of the genome projects, the complete sequence of the human genome, is finished. This project reveals the complete sequence of the 3 billion bases and the relative positions of all estimated 30.000 genes in this genome. Having this sequence opens unlimited possibilities for the elucidation of gene function and interaction of different genes. In recent years a systematic effort (SNP 20 consortium) has been underway to identify single nucleotide polymorphisms (SNPs) throughout the human genome and so far several million of these differences between different human beings have been identified (dbSNP contained 5.5 million SNPs in October 2003).

25 Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI) has revolutionized the mass spectrometric analysis of biomolecules (Karas, M. & Hillenkamp, F. *Anal. Chem.* **60**, 2299-2301 (1988)). The field of DNA analysis by mass spectrometry was recently extensively reviewed by Tost and Gut (Mass Spectrometry Reviews, **21**, 388-418 (2002)) and Sauer and Gut (Journal of Chromatography B, **782**, 73-87, (2002)). MALDI has been applied to the analysis 30 of DNA in variations that range from the analysis of PCR products to approaches using allele-specific termination to single nucleotide primer extension reactions and sequencing (Liu, Y.-H., et al. *Rapid Commun. Mass Spectrom.* **9**, 735-743 (1995);

Ch'ang, L.-Y., *et al. Rapid Commun. Mass Spectrom.* **9**, 772-774 (1995); Little, D.P., *et al. J. Mol. Med.* **75**, 745-750 (1997); Haff, L. & Smirnov, I.P. *Genome Res.* **7**, 378-388 (1997), Fei, Z., Ono, T. & Smith, L.M. *Nucleic Acids Res.* **26**, 2827-2828 (1998); Ross, P., Hall, L., Smirnov, I. & Haff, L. *Nature Biotech.* **16**, 1347-1351 (1998); Ross, P.L., Lee, K. & Belgrader, P. *Anal. Chem.* **69**, 4197-4202 (1997); Griffin, T.J., Tang, W. & Smith, L.M. *Nature Biotech.* **15**, 1368-1372 (1997); Köster, H., Higgins, G.S & Little, D.P. US Patent 6,043,031). These methods are used to genotype previously identified mutations, SNPs, or insertion/deletions (indels). Spin column purification and/or magnetic bead technology, reversed-phase purification, or ion-exchange resins are frequently applied prior to mass spectrometric analysis.

The GOOD assay (IG Gut et S. Beck: US 6,268,812 ; IG Gut et al: US 6,503,710) is a method for SNP genotyping that uses MALDI mass spectrometry for detection (Sauer et al. 28, e13 and e100 (2000)). Allele-distinction is based on primer extension. In order to make products more amenable to MALDI analysis a substantial part of the primer is removed prior to mass spectrometric analysis. A further element that is included is charge tagging. This means that the final product is conditioned such that it carries either a single positive or a single negative charge. Generally this is achieved by alkylation of a phosphorothioate backbone and in some instances including a quaternary ammonium group to the penultimate base of the primer. The attachment of the quaternary ammonium group gives options for the design of multiplexes - individual SNPs can be moved up or down in the mass spectrum to achieve optimal resolution and separation.

The major histocompatibility complex (MHC) of humans is a cluster of genes on chromosome 6p21. It is of greatest importance as many diseases show association with genes in this region of the genome. All human leukocyte antigen (HLA) coding genes are found in the MHC. The HLA genes are highly variable and implicated in tissue transplantation, immunity and autoimmune disease such as diabetes, psoriasis, lupus, Crohn's disease, colitis, arthritis, and others. The HLA class I genes are HLA-A, HLA-B, HLA-C, The HLA class II genes are HLA-DR, HLA-DQ, HLA-DP,....

HLA typing methods differ dramatically in their approaches. Serological tests can be carried out but have only limited resolution. In the last 15 years the DNA sequence of the MHC has been extensively studied and high resolution typing now makes use of a wealth of DNA sequence information. Methods for DNA based HLA typing range from SSA (sequence specific amplification) where combinations of primers that are specific for different alleles are used to carry out PCR (US 5,545,526). Primers are combined in a way that the sizing of the PCR products allows unambiguous assignment of present base combinations. Multiple combinations are used to identify HLA types. The procedure works its way through a tree of combinations starting with a grouping into rough classes from where on further tests are carried out with specific reagents to subdivide in a class. This method is also known as SSP (sequence specific primers). An alternative method is termed SSOP (sequence specific oligonucleotide probes; US 6,503,707). Here a locus specific PCR is carried out followed by hybridisation with sequence specific oligonucleotide probes. As sequencing technology (and in particular the software for sequence calling) has dramatically improved over the last decade it now is also possible to gain a good degree of identification of HLA types by sequencing (WO 98/35059). Effectively a locus-specific PCR product is sequenced. Problems that arise here are that heterozygous individuals occasionally give rise to ambiguous haplotype calls that can not be resolved (Robinson, J.; Waller, M.J.; Marsh, St.G.E.: "Exon Identities and Ambiguous Typing Combinations"; IMGT/HLA Database; October 2003). The inclusion of allele-specific PCR helps achieve certainty. Resolution requires multiple products per locus to be generated and sequenced. However, as sequencing results can be very convoluted the interpretation in absence of allele-specific PCR can be cumbersome. All together the sequence-based typing requires many iterations in application. Reference strand mediated conformation analysis (RSCA) is a method used to study samples that potentially have a previously unknown sequence in their HLA (Correl et al., *Tissue Antigens* 56, 82-86, 2000). For a recent review for the reasoning of HLA typing as well as methodological advances see Petersdorf et al. (*Tissue Antigens*, 61, 1-11, 2003).

The inventors have thus set themselves the task of providing an easy method for the simultaneous capture of all parental mini-haplotypes in highly polymorphic regions of genomes. The procedure has to be executable on a cost-effective genotyping platform. The method should be particularly applicable for HLA typing. It is an aim 5 to resolve frequent and rare HLA alleles as well as possible.

The object of the present invention is a method for HLA typing by the unambiguous determination of short DNA sequence elements (2-6 bases) simultaneously on both 10 parental alleles at a selected number of positions in HLA genes, comprised of the steps for each position of a) hybridising a combination of oligonucleotides (primer pool) complementary to all known sequence variants to a DNA strand upstream of a given position; b) carrying out a primer extension reaction with at least one of the four dNTP substrates substituted by a terminating analog; c) analysing the products by mass spectrometry, with the resulting masses allowing unambiguous 15 identification of the used primers and the added bases.

In the present invention:

- "HLA" means the human leukocyte antigen locus on chromosome 6p21, consisting of HLA genes (HLA-A, HLA-B, HLA-C, HLA-DRB1,...) that are 20 used to determine the degree of matching, for example, between a recipient and a donor of a tissue graft.
- "HLA typing" means the identification of a known HLA allele of a given locus (HLA-A, HLA-B, HLA-C, HLA-DRB1,...).
- "HLA allele" means a nucleotide sequence within a locus on one of the two 25 parental chromosomes.
- "HLA-A" means the DNA sequence of exons 2 and 3 of the HLA-A gene.
- "HLA-B" means the DNA sequence of exons 2 and 3 of the HLA-B gene.
- "HLA-DRB1" means the DNA sequence of exon 2 of the HLA-DRB1 gene.
- "Polymorphism" means individual positions in a DNA sequence that exist in 30 different variants.
- "Haplotype" means the DNA sequence of one of the two alleles in a give region of the genome.

- "Mini-haplotype" means 2-6 contiguous bases on one parental allele.
- "Primer pools" or "pools of primers" means sets of primers that are used in one primer extension reaction. For each known HLA allele at least one primer is in the pool that is completely complementary in sequence. This assures perfect annealing. Mismatches that are more than 4 bases from the 3'end of the primer do not affect the results of the GOOD assay, as all of those bases are removed by 5'phosphodiesterase after the primer extension reaction. Primers of the pool containing mismatches in the last few bases are not extended by the DNA polymerase and thus not observable.
- 10 - "MALDI mass spectrometer" means a mass spectrometer that uses matrix-assisted laser desorption/ionization for the volatilisation of a sample and time-of-flight analysis for mass separation.
- "Subgroup" means alleles, which are identical after the mini-haplotyping of the first set of selected positions. For the high resolution typing we resolve
- 15 subgroups generated with 10 mini-haplotyping reactions. The criteria for resolving subgroups are: a) they still contain alleles with different two-digit types, b) subgroups with more than four alleles, and c) subgroups with frequent alleles (see list below).

20 Here we show a methodology for the determination of sequence motifs of 2-6 bases in very polymorphic regions of genomes. In principle this methods equates to the determination of mini-haplotypes of 2-6 bases. The individual parental mini-haplotypes can be determined in one reaction without ambiguities. This methodology is applied to a chosen set of positions for HLA typing of HLA-A,

25 HLA-B, and HLA-DRB1. The sets disclosed here have different purposes. First sets of 19, 19, and 10 positions are suggested to distinguish a maximum of HLA alleles in HLA-A, HLA-B, and HLA-DRB1, respectively, with respect to differentiating alleles that are frequent in the general population from ones that are rare. The frequent alleles that were screened for are A*0101, A*0201, A*0301, A*2301,

30 A*2402, A*2902, A*3001 and A*3002 for HLA-A, B*0702, B*0801, B*1302, B*1501, B*1801, B*3501, B*3503, B*4001, B*4402, B*4403, B*5101 and B*5701 for HLA-B, and DRB1*0101, DRB1*0301, DRB1*0401, DRB1*0701,

DRB1*1101, DRB1*1104, DRB1*1302 and DRB1*1501 for HLA-DRB1. This set of markers provides unambiguous identification of frequent HLA alleles with 93.4 - 100 % certainty in HLA-A, 97.6 - 100 % in HLA-B, and 97.2 - 100 % in HLA-DRB1.

5 A second set of 10 positions each in HLA-A, HLA-B, and HLA-DRB1, respectively are described that provide a maximum number of subgroups, that can then be further resolved by the addition of a set of subgroup specific positions. Again the ten positions in each locus were chosen on the basis of providing best distinction between the frequent HLA alleles listed above from the rest of the HLA
10 alleles (rare). This resulted in groups containing 2-30 HLA alleles depending on the locus. Within each group a number of positions can be tested to provide resolution between the HLA alleles within the group. The number of positions that have to be additionally analysed range from 1-25 in order to achieve 4-digit resolution. With this technology HLA typing can be carried out at a substantially reduced cost with a
15 proven high-throughput detection platform (MALDI mass spectrometry).

In a preferred embodiment of the method of the invention, the DNA strand of step a) is produced by a DNA replication procedure such as PCR or rolling circle replication.

20 A set of locus-specific PCR reactions for the selective amplification of each locus is described by the International Histocompatibility Working Group, Technical Manuals (www.ihwg.org/tmanual/Tmcontents.htm).

In a very preferred embodiment of the method of the invention, a combination of primers (pools of primers) contains slightly varying sequences so that all known
25 sequences of the HLA alleles are accommodated by a perfectly matching primer.

The pool of primers guarantees that at least one primer is perfectly matched. The hybridised oligonucleotides of the primer pool are extended onto a polymorphic position. A requirement is that the added base together with the base composition of the primer gives a unique mass. The detection of this mass in the mass
30 spectrometric profile indicates the presence of a sequence containing both the complementary sequence of the primer and the added base. In order to make all primers of a primer pool distinguishable by mass it is possible to add different mass

shifting agents to the primers. The easiest way to accomplish this is by using charge/mass tagging technology such as is used in the GOOD assay. The penultimate base from the 3'end of the primer is amino-modified and used to add tags via NHS-ester chemistry. The pools of primers of course contain primers that

5 sometimes differ by as little as one base. Sequences identical in base content can still be distinguished by the suitable selection of mass tags. Also, we have found that a primer carrying a mismatch in the last eight bases from the 3'end even if it anneals is not extended by the polymerase and thus screened out. This might be due to insufficient hybridisation or a resistance of the DNA polymerase to attach or

10 extend when a mismatch is present. We thus make use of two effects for our mini-haplotyping: 1) allele-specific hybridisation and 2) allele-specific primer extension. Mismatches that are further than four bases away from the 3'end of the extension primer do not result in increased complexity of the mass spectra as they are removed in the 5'phosphodiesterase digestion step of the GOOD assay.

15 In a preferred embodiment of the method of the invention, mass shifting tags are added to the individual primers sequences of a primer pool to make them uniquely distinguishable once the terminating base is added.

In another preferred embodiment of the method of the invention, termination products for known alleles are generated by extending the perfectly hybridised

20 primer with a combination of dNTPs and ddNTPs or analogues thereof with a DNA polymerase to generate specific termination products to make them uniquely distinguishable by their mass.

25 In a preferred embodiment of the method of the invention, the GOOD assay is used. It typically applies single base primer extension, thus only the four terminating bases (ddNTPs) or synthetic analogues with the same qualities in terms of DNA polymerase tolerance are used for primer extension. α -S-ddNTPs are very suitable analogues.

30 In a preferred embodiment of the method of the invention, mass spectrometry, in particular MALDI or ESI mass spectrometry is used for analysis of the masses of products.

For HLA typing a set of said mini-haplotyping assays has to be carried out to achieve sufficient information content.

For HLA typing of HLA-A the preferred set of assays are those of positions 98, 414, 539, 282, 571, 368, 256, 292, 238, 270, 453, 527, 502, 81, 268, 559, 92, 123 and 396 (according to the numbering of the HLA-A gene starting at cDNA sequence position 1 of exon 1; see Figure 1). This results in medium resolution 5 HLA typing. The input criteria for the selection are the frequency of HLA alleles. Some HLA types are identified unambiguously.

For HLA typing of HLA-B accordingly the following positions are preferably analysed by mini-haplotyping assays to achieve medium resolution: 539, 419, 559, 412, 272, 362, 302, 363, 206, 369, 259, 97, 583, 292, 222, 527, 418, 435 and 571 10 (according to the numbering of the HLA-B gene starting at cDNA sequence position 1 of exon 1; see Figure 2).

For HLA typing of HLA-DRB1 accordingly the following positions are preferably analysed by mini-haplotyping to achieve medium resolution: 125, 196, 197, 227, 261, 286, 299, 308, 341 and 345 (according to the numbering of the HLA-DRB1 15 gene starting at cDNA sequence position 1 of exon 1; see Figure 3).

In a preferred embodiment for high resolution HLA typing of HLA-A positions 98, 414, 539, 282, 571, 368, 256, 292, 238 and 270 (according to the numbering of the HLA-A gene starting at cDNA sequence position 1 of exon 1; see Figure 4) are used for mini-haplotyping to generate sub-groups (HLA-A_A, HLA-A_B, HLA- 20 A_C, HLA-A_D, HLA-A_E, HLA-A_F, HLA-A_G, HLA-A_H, HLA-A_I, HLA- A_J, HLA-A_K, HLA-A_L, HLA-A_M, HLA-A_N, and HLA-A_O; see Table I).

Positions 224, 268, 376, 502, 561 and 616 are preferably analysed to resolve subgroup HLA-A_A (sequences identical over exons 2 and 3 for alleles A*29010101 and A*29010102); positions 126 and 526 to resolve subgroup HLA- 25 A_B; positions 81, 90, 92, 212, 214, 257, 265, 299, 302, 404, 420, 427, 453, 485, 489 and 502 to resolve subgroup HLA-A_C (sequences identical over exons 2 and 3 for alleles A*24020101, A*24020102L, A*240203, A*2409N and A*2411N); positions 160, 200, 362 and 524 to resolve subgroup HLA-A_D; positions 180, 299, 301, 302, 346, 418, 453, 517, 524, 526, 527, 557, 559 and 560 to resolve subgroup 30 HLA-A_E; positions 299, 301, 302, 341 and 583 to resolve subgroup HLA-A_F; positions 127, 341, 399, 480, 502, 503, 524, 526, 527, 553, 559, 560 and 565 to resolve subgroup HLA-A_G; positions 228, 233, 463, 519, 530 and 583 to resolve

subgroup HLA-A_H; positions 102, 275, 317, 362, 418, 419, 497, 524, 555, 595 and 618 to resolve subgroup HLA-A_I (sequences identical over exons 2 and 3 for alleles A*680102 and A*6811N); positions 92, 331, 453, 524, 559, 560 and 564 to resolve subgroup HLA-A_J; positions 78, 81, 123, 125, 142, 144, 194, 268, 294, 5 324, 355, 362, 396, 403, 419, 453, 456, 477, 493, 517, 524, 526, 527, 559 and 560 to resolve subgroup HLA-A_K (sequences identical over exons 2 and 3 for alleles A*02010101, A*02010102, A*020108, A*0209, A*0243N and A*0266); positions 113, 299, 301, 302, 308, 311, 523, 524 to resolve subgroup HLA-A_L; positions 171, 363, 498 and 559 to resolve subgroup HLA-A_M; positions 376, 426, 527, 10 555, 557 and 595 to resolve subgroup HLA-A_N; position 299 to resolve subgroup HLA-A_O.

TABLE I

| Subgroups of HLA-A | Alleles of Subgroups | Positions to resolve Subgroups |
|--------------------|--|---|
| HLA-A_A | A*29010101, A*29010102, A*290201, A*290202, A*2904, A*2906, A*2908N, A*2909 | 224, 268, 376, 502, 561, 616 |
| HLA-A_B | A*3002, A*3009, A*3012 | 126, 526 |
| HLA-A_C | A*24020101, A*24020102L, A*240202, A*240203, A*240204, A*2404, A*2405, A*2408, A*2409N, A*2411N, A*2420, A*2421, A*2425, A*2426, A*2427, A*2429, A*2432, A*2435, A*2436N, A*2437, A*2438, A*2439 | 81, 90, 92, 212, 214, 257, 265, 299, 302, 404, 420, 427, 453, 485, 485, 489, 502 |
| HLA-A_D | A*0206, A*0214, A*0221, A*0251, A*0257 | 160, 200, 362, 524 |
| HLA-A_E | A*250101, A*250102, A*2601, A*2604, A*2605, A*2609, A*2610, A*2611N, A*2612, A*2614, A*2615, A*2617, A*2618, A*6603 | 180, 299, 301, 302, 346, 418, 453, 517, 524, 526, 527, 557, 559, 560 |
| HLA-A_F | A*2502, A*2613, A*6601, A*6602, A*6604 | 299, 301, 302, 341, 583 |
| HLA-A_G | A*110101, A*110102, A*1102, A*1103, A*1104, A*1105, A*1107, A*1109, A*1112, A*1113, A*1114, A*1115 | 127, 341, 399, 480, 502, 503, 524, 526, 527, 553, 559, 560, 565 |
| HLA-A_H | A*3301, A*330301, A*330302, A*3304, A*3305, A*3306, A*3307 | 228, 233, 463, 519, 530, 583 |
| HLA-A_I | A*680101, A*680102, A*680103, A*6807, A*6811N, A*6812, A*6816, A*6817, A*6819, A*6821, A*6822, A*6823, A*6824 | 102, 275, 317, 362, 418, 419, 497, 524, 555, 595, 618 |
| HLA-A_J | A*2301, A*2303, A*2305, A*2306, A*2307N, A*2308N, A*2310, A*2413 | 92, 331, 453, 524, 556, 560, 564 |
| HLA-A_K | A*02010101, A*02010102, A*020102, A*020103, A*020104, A*020105, A*020106, A*020107, A*020108, A*020109, A*0204, A*0209, A*0216, A*0224, A*0225, A*0226, A*0229, A*0230, A*0231, A*0232N, 0A*0240, A*0242, A*0243N, A*0258, A*0259, A*0260, A*0264, A*0266, A*0267, A*0253N | 78, 81, 123, 125, 142, 144, 194, 268, 294, 324, 355, 362, 396, 403, 419, 453, 419, 453, 456, 477, 493, 517, 524, 526, 527, 559, 560 |
| HLA-A_L | A*3201, A*3203, A*3206, A*7401, A*7402, A*7403, A*7408, A*7409 | 113, 299, 301, 302, 308, 311, 523, 524 |
| HLA-A_M | A*010101, A*010102, A*0103, A*0104N, A*0108, A*0109 | 171, 363, 498, 559 |
| HLA-A_N | A*03010101, A*03010102, A*0303N, A*0304, A*0305, A*0306, A*0307, A*0311N | 376, 426, 527, 555, 557, 595 |
| HLA-A_O | A*2504, A*2608 | 299 |

In a preferred embodiment for high resolution, HLA typing of HLA-B positions 539, 419, 559, 412, 272, 362, 302, 363, 206 and 369 (according to the numbering of the HLA-B gene starting at cDNA sequence position 1 of exon 1; see Figure 5) are used for mini-haplotyping to generate sub-groups (HLA-B_A, HLA-B_B, HLA-B_C, 5 HLA-B_D, HLA-B_E, HLA-B_F, HLA-B_G, HLA-B_H, HLA-B_I, HLA-B_J, HLA-B_K, HLA-B_L, HLA-B_M, HLA-B_N, HLA-B_O, HLA-B_P, HLA-B_Q, HLA-B_R, HLA-B_S, HLA-B_T, HLA-B_U, HLA-B_V, HLA-B_W, HLA-B_X, -HLA-B_Y, HLA-B_Z, HLA-B_AA, HLA-B_AB and HLA-B_AC ; see Table II). Positions 259, 341 and 473 are preferably analyzed to resolve subgroup HLA-B_A 10 (sequences identical over exons 2 and 3 for alleles B*0801 and B*0819N); positions 106, 144, 222, 259, 273, 311, 313, 418, 445, 493, 528 and 540 to resolve subgroup HLA-B_B (sequences identical over exons 2 and 3 for alleles B*44020101, B*44020102, B*4419N and B*4427); positions 319, 416, 545 and 572 to resolve subgroup HLA-B_C; positions 106, 131, 165, 215, 243, 277, 292, 322, 481, 582, 603 15 and 616 to resolve subgroup HLA-B_D; positions 106, 146, 165, 181, 238, 259, 263, 292, 328.1/329(insert for B*1579N), 379, 435, 453, 463, 485, 526, 571, 572 and 583 to resolve subgroup HLA-B_E (sequences identical over exons 2 and 3 for alleles B*15010101 and B*15010102); positions 142, 171, 255, 257, 395, 430, 544, 566 and 572 to resolve subgroup HLA-B_F; positions 117, 247, 248, 277, 345, 418, 489 and 20 527 to resolve subgroup HLA-B_G (sequences identical over exons 2 and 3 for alleles B*270502, B*270504 and B*2713); positions 134, 141, 200, 213, 259, 304 and 527 to resolve subgroup HLA-B_H; positions 83, 141, 211, 222, 242, 322, 404, 414, 435, 463, 502, 527, 544, 571, 572 and 583 to resolve subgroup HLA-B_I (sequences identical over exons 2 and for alleles B*510101, B*510105, B*5111N, B*5130 and B*5132); positions 103, 142, 222, 243, 259, 292, 477, 486 and 499 to resolve subgroup HLA-B_J (sequences identical over exons 2 and 3 for alleles B*400101 and B*400102); positions 103, 259, 292, 295, 527 and 583 to resolve subgroup HLA-B_K (sequences identical over exons 2 and 3 for alleles B*180101 and B*1817N); positions 320 and 500 to resolve subgroup HLA-B_L; positions 311, 527 and 583 to 25 resolve subgroup HLA-B_M; positions 119, 292, 259, 319, 425, 527, 546 and 583 to resolve subgroup HLA-B_N (sequences identical over exons 2 and 3 for alleles B*350101, B*3540N and B*3542); positions 97, 142, 245 and 527 to resolve subgroup HLA-B_O; positions 97 and 175 to resolve subgroup HLA-B_P; positions 30

TABLE II

| <u>Subgroups of</u> <u>HLA-B</u> | <u>Alleles of the subgroup</u> | <u>Positions to resolve</u> <u>Subgroups</u> |
|-------------------------------------|--|--|
| HLA-B_A | B*0801, B*0808N, B*0810, B*0818, B*0819N | 259, 341, 473 |
| HLA-B_B | B*44020101, B*44020102S, B*440202, B*440203, B*4405, B*4411, B*4412, B*4419N, B*4422, B*4423N, B*4424, B*4425, B*4427, B*4433, B*4434, B*4435 | 106, 144, 222, 259, 273, 311, 313, 418, 445, 493, 528, 540 |
| HLA-B_C | B*4415, B*4501, B*4503, B*4504, B*4505 | 319, 416, 545, 572 |
| HLA-B_D | B*070201, B*070202, B*070203, B*070204, B*0703, B*0716, B*0721, B*0722, B*0723, B*0729, B*0730, B*0733, B*0735 | 106, 131, 165, 215, 243, 277, 292, 322, 481, 582, 603, 616 |
| HLA-B_E | B*15010101, B*15010102, B*150102, B*150103, B*150104, B*1512, B*1514, B*1515, B*1519, B*1528, B*1533, B*1534, B*1538, B*1560, B*1570, B*1571, B*1575, B*1578, B*1579N, B*1581, B*1582 | 106, 146, 165, 181, 238, 259, 263, 292, 328.1/329, 379, 435, 453, 463, 485, 526, 571, 572, 583 |
| HLA-B_F | B*440301, B*4413, B*4426, B*4429, B*4430, B*4432, B*4436, B*4437, B*4438, B*4439 | 142, 171, 255, 257, 395, 430, 544, 566, 572 |
| HLA-B_G | B*2703, B*270502, B*270503, B*270504, B*270505, B*270506, B*2709, B*2710, B*2713, B*2716, B*2717 | 117, 247, 248, 277, 345, 418, 489, 527 |
| HLA-B_H | B*5107, B*520101, B*520102, B*520103, B*520104, B*5203, B*5204, B*5205 | 134, 141, 200, 213, 259, 304, 527 |
| HLA-B_I | B*510101, B*510102, B*510103, B*510104, B*510105, B*510201, B*510202, B*5103, B*5109, B*5111N, B*5112, B*5114, B*5118, B*5119, B*5123, B*5124, B*5126, B*5127N, B*5128, B*5130, B*5132, B*5133 | 83, 141, 211, 222, 242, 322, 404, 414, 435, 463, 502, 527, 544, 571, 572, 583 |
| HLA-B_J | B*400101, B*400102, B*400103, B*4010, B*4011, B*401401, B*401402, B*401403, B*4022N, B*4025, B*4043 | 103, 142, 222, 243, 259, 292, 477, 486, 499 |
| HLA-B_K | B*180101, B*180102, B*1803, B*1804, B*1805, B*1811, B*1812, B*1815, B*1817N | 103, 259, 292, 295, 527, 583 |
| HLA-B_L | B*570101, B*5706, B*5708 | 320, 500 |
| HLA-B_M | B*3527, B*5301, B*5302, B*5306, B*5308 | 311, 527, 583 |
| HLA-B_N | B*350101, B*350102, B*3507, B*3510, B*3511, B*3521, B*3524, B*3529, B*3540N, B*3541, B*3542, B*5305 | 119, 292, 259, 319, 425, 527, 546, 583 |
| HLA-B_O | B*5501, B*5502, B*5505, B*5510, B*5516 | 97, 142, 245, 527 |
| HLA-B_P | B*5401, B*5402, B*5507 | 97, 175 |

| | | |
|----------|--|--|
| HLA-B_Q | B*3910, B*670101, B*670102 | 246, 277 |
| HLA-B_R | B*3803, B*390201, B*390202, B*3913, B*3923 | 246, 292, 311, 503 |
| HLA-B_S | B*3801, B*380201, B*380202, B*3804, B*3805, B*3809 | 103, 261, 309, 311, 474 |
| HLA-B_T | B*390101, B*390103, B*390104, B*3904, B*3905, B*3912, B*3922, B*3925N, B*3926 | 97, 103, 106, 243, 259, 292, 404, 524 |
| HLA-B_U | B*3503, B*3513, B*3536 | 259, 320 |
| HLA-B_V | B*0734, B*5504 | 106 |
| HLA-B_W | B*4047, B*4431 | 97 |
| HLA-B_X | B*4002, B*4027, B*4029, B*4035, B*4040, B*4045 | 97, 106, 257, 418, 463 |
| HLA-B_Y | B*400104, B*4004 | 106 |
| HLA-B_Z | B*4012, B*4046, B*4803 | 106, 144 |
| HLA-B_AA | B*2703, B*270502, B*270503, B*270504, B*270505, B*270506, B*2709, B*2710, B*2713, B*2716, B*2717 | 117, 247, 248, 283, 345, 418, 489, 527 |
| HLA-B_AB | B*1562, B*4802 | 106 |
| HLA-B_AC | B*1302, B*1308 | 548 |

246 and 277 to resolve subgroup HLA-B_Q; positions 246, 292, 311 and 503 to resolve subgroup HLA-B_R; positions 103, 261, 309, 311 and 474 to resolve subgroup HLA-B_S; positions 97, 103, 106, 243, 259, 292, 404 and 524 to resolve subgroup HLA-B_T (sequences identical over exons 2 and 3 for alleles B*390101 and B*390103); positions 259 and 320 to resolve subgroup HLA-B_U; position 106 to resolve HLA-B_V; positions 97 to resolve HLA-B_W; positions 97, 106, 257, 418 and 463 to resolve HLA-B_X; position 106 to resolve HLA-B_Y; positions 106 and 144 to resolve HLA-B_Z; positions 117, 247, 248, 283, 345, 418, 489, and 527 to resolve HLA-B_AA; positions 106 to resolve HLA-B_AB; positions 548 to resolve HLA-B_AC.

In a preferred embodiment, the method for HLA typing resolves groups A-P of HLA-DRB1.

For high resolution, HLA typing of HLA-DRB1 positions are: 125, 196, 197, 227, 15 261, 286, 299, 308, 341 and 345 (according to the numbering of the HLA-DRB1 gene starting at DNA sequence position 1 of exon 1; see Figure 6) are used for mini-haplotyping to generate sub-groups (HLA-DRB1_A, HLA-DRB1_B, HLA-DRB1_C, HLA-DRB1_D, HLA-DRB1_E, HLA-DRB1_F, HLA-DRB1_G, HLA-DRB1_H, HLA-DRB1_I, HLA-DRB1_J, HLA-DRB1_K, HLA-DRB1_L, HLA-DRB1_M, 20 HLA-DRB1_N, HLA-DRB1_O, HLA-DRB1_P; see Table III).

In a very preferred embodiment, positions 123, 174, 250, 278 and 317 are analysed to resolve subgroup HLA-DRB1_A; positions 192, 203, 256 and 259 to resolve subgroup HLA-DRB1_B; 256, 260, 317 and 351 to resolve subgroup HLA-DRB1_C; positions 155, 204, 233, 239, 256, 304, 357 and 366 to resolve subgroup HLA-DRB1_D; positions 122, 171, 257 and 317 to resolve subgroup HLA-DRB1_E; positions 164, 167, 171, 230, 235, 306, 317, 321 and 337 to resolve subgroup HLA-DRB1_F; positions 164, 257, 266 and 303 to resolve subgroup HLA-DRB1_G; positions 164, 181, 188, 220, 229, 256, 266, 317 and 318 to resolve subgroup HLA-DRB1_H; position 257 to resolve subgroup HLA-DRB1_I; positions 181, 239 and 357 to resolve subgroup HLA-DRB1_J; positions 122, 144, 239, 303, 317, 318 and 321 to resolve subgroup HLA-DRB1_K (sequences identical over exons 2 and 3 for alleles DRB1*110101 and DRB1*110102); positions 118, 161, 257, 260, 318 and 321 to resolve subgroup HLA-DRB1_L; positions 165, 257, 293 and 303 to resolve subgroup HLA-DRB1_M (sequences identical over exons 2 and 3 for alleles DRB1*120101 and DRB1*1206); positions 177, 240, 256, 257 and 357 to resolve subgroup HLA-DRB1_N; positions 150 175, 230, 236 and 321 to resolve subgroup HLA-DRB1_O (sequences identical over exons 2 and 3 for alleles DRB1*150101 and DRB1*1513); positions 115, 220 and 317 to resolve subgroup HLA-DRB1_P.

Another object of the invention is a kit to carry out the procedure. It consists of pooled combinations of primers. The primers that are used in the pools for HLA-A, HLA-B, and HLA-DRB1 and the masses of the genotyping products are listed in Tables IV, V, and VI respectively. CT refers to the mass shifting mass tag that is attached to that primer of the pool.

Another object of the invention is the use of the method of the invention for screening of tissue donors.

In a preferred embodiment, the use is for bone marrow donors in registries for screening of frequent and rare HLA types.

Still another object of the invention is the use of the primers represented in Table IV, V and VI to carry out HLA typing.

TABLE III

| Subgroups of HLA-DRB1 | Alleles of Subgroups | Positions to resolve Subgroups |
|-----------------------|--|---|
| HLA-DRB1_A | DRB1*070101, DRB1*070102, DRB1*0703, DRB1*0704, DRB1*0705, DRB1*0707 | 123, 174, 250, 317 |
| HLA-DRB1_B | DRB1*040101, DRB1*040102, DRB1*0409, DRB1*0426, DRB1*0433 | 192, 203, 256, 259 |
| HLA-DRB1_C | DRB1*0404, DRB1*0410, DRB1*0423, DRB1*0440, DRB1*0444 | 256, 260, 317, 351. |
| HLA-DRB1_D | DRB1*040501, DRB1*040502, DRB1*040503, DRB1*040504, DRB1*0408, DRB1*0429, DRB1*0430, DRB1*0445, DRB1*0448 | 155, 204, 233, 239, 256, 304, 357, 366 |
| HLA-DRB1_E | DRB1*1402, DRB1*1409, DRB1*1413, DRB1*1446, DRB1*1447, DRB1*1448 | 122, 171, 257, 317 |
| HLA-DRB1_F | DRB1*130101, DRB1*130102, DRB1*130103, DRB1*1315, DRB1*1327, | 164, 167, 171, 230, 235, 306, 317, 321, 337 |
| HLA-DRB1_G | DRB1*130201, DRB1*130202, DRB1*1331, DRB1*1339, DRB1*1341 | 164, 257, 266, 303 |
| HLA-DRB1_H | DRB1*030101, DRB1*030102, DRB1*0307, DRB1*0312, DRB1*0313, DRB1*0315, DRB1*0316, DRB1*0318, DRB1*0322, DRB1*0323 | 164, 181, 188, 220, 229, 256, 266, 317, 318 |
| HLA-DRB1_I | DRB1*1137, DRB1*1425 | 257 |
| HLA-DRB1_J | DRB1*110401, DRB1*110402, DRB1*1143, DRB1*1146 | 181, 239, 357 |
| HLA-DRB1_K | DRB1*110101, DRB1*110102, DRB1*110103, DRB1*110104, DRB1*110105, DRB1*112701, DRB1*112702, DRB1*1130, DRB1*1139 | 122, 144, 239, 303, 317, 318, 321 |
| HLA-DRB1_L | DRB1*1117, DRB1*140101, DRB1*140102, DRB1*1408, DRB1*1426, DRB1*1438, DRB1*1439 | 118, 161, 257, 260, 318, 321 |
| HLA-DRB1_M | DRB1*120101, DRB1*120102, DRB1*1206, DRB1*1207, DRB1*1208, DRB1*1209 | 165, 257, 293, 303 |
| HLA-DRB1_N | DRB1*080101, DRB1*080102, DRB1*080201, DRB1*080202, DRB1*080203, DRB1*0807, DRB1*0811 | 177, 240, 256, 257, 357 |
| HLA-DRB1_O | DRB1*150101, DRB1*150103, DRB1*150105, DRB1*1503, DRB1*1506, DRB1*1509, DRB1*1513 | 150, 175, 230, 236, 321 |
| HLA-DRB1_P | DRB1*010101, DRB1*0105, DRB1*0107, DRB1*0111 | 115, 220, 317 |

16
TABLE IV

| No. | Name | Sequence | CT | Primer Masses | A | C | G | T | |
|-----|----------------|-----------------------------|-----------------------------|---------------|--------|--------|--------|--------|---|
| 1 | HLAA_811_1f20 | TGCTCGCCCCCAGGCTCCspC^spA | 0 | 1098,1 | 1425,1 | 1401,3 | - | - | |
| 2 | HLAA_812_1f20 | TGCTCGCCCCCAGGCTCTspC^spA | 0 | 1113,1 | - | 1416,3 | 1452,4 | - | |
| 3 | HLAA_921_1f20 | AGGCTCCCACATCCATGAGspC^spT | 0 | 1129,1 | 1456,4 | - | - | - | |
| 4 | HLAA_922_1f20 | AGGCTCCCACATCCATGAGspG^spT | 0 | 1169,1 | 1496,4 | - | 1512,4 | - | |
| 5 | HLAA_923_1f20 | AGGCTCTCASTCCATGAGspG^spT | 0 | 1169,1 | 1496,4 | - | 1512,4 | - | |
| 6 | HLAA_981_1f20 | CCACTCCATGAGGTATTTspC^spA | 0 | 1113,1 | - | 1416,3 | - | - | |
| 7 | HLAA_982_1f20 | CCACTCCATGAGGTATTTspC^spT | 0 | 1104,1 | 1431,4 | 1407,3 | - | 1422,3 | |
| 8 | HLAA_1231_2r20 | GCGATGAAGCGGGGCTCspCspT^spC | 0 | 1510,5 | - | - | 1853,8 | - | |
| 9 | HLAA_1232_2r20 | GCGATGAAGCGGGGCTCspTspC^spC | -28 | 1380,4 | 1707,7 | - | - | - | |
| 10 | HLAA_1233_2r20 | GCGATGAAGCGGGGCTTspCspC^spC | 0 | 1408,4 | - | - | 1751,6 | - | |
| 11 | HLAA_1234_2r20 | GMGATGAAGCGGGGCTCspCspC^spC | 0 | 1393,4 | 1720,7 | - | 1736,7 | - | |
| 12 | HLAA_2381_2r20 | CTSGTCCAATACTCCGspGspA^spC | 0 | 1497,4 | - | 1800,6 | - | - | |
| 13 | HLAA_2382_2r20 | CYCGTCCAATACTCCGspGspA^spC | 0 | 1497,4 | - | 1800,6 | - | - | |
| 14 | HLAA_2383_2r20 | CTCGTCCAATACTCCGspGspC^spT | 0 | 1488,4 | - | 1791,6 | - | 1806,4 | |
| 15 | 15 | HLAA_2384_2r20 | CTSGTCCAATACTCAAGspGspC^spC | 0 | 1473,4 | - | 1776,6 | - | - |
| 16 | HLAA_2385_2r20 | CYGGTCCAATACTCCGspGspC^spC | 0 | 1473,4 | - | 1776,6 | - | - | |
| 17 | HLAA_2386_2r20 | CMGGTCCAATACTCCGspGspC^spC | 0 | 1473,4 | - | 1776,6 | - | - | |
| 18 | HLAA_2387_2r20 | CYCGTCCAATACTCCGspGspC^spC | 0 | 1473,4 | - | 1776,6 | - | - | |
| 19 | HLAA_2561_1r19 | CTTCATATTCCGTGTCTCspC^spT | 0 | 1089,1 | - | 1392,3 | 1432,4 | - | |
| 20 | HLAA_2562_1r19 | CTTCACWTTCCGTGTCTCspC^spT | 0 | 1089,1 | - | 1392,3 | 1432,4 | - | |
| 21 | HLAA_2563_1r19 | CTTCACATKCCGTGTCTGspC^spA | 0 | 1138,1 | - | - | 1481,4 | - | |
| 22 | HLAA_2564_1r19 | CTTCACTTCCGTGTGTTspC^spC | 0 | 1089,1 | - | - | 1432,1 | - | |
| 23 | HLAA_2565_1r19 | CYTCACATTCCGTGTGTTspC^spC | 0 | 1089,1 | - | - | 1432,1 | - | |
| 24 | HLAA_2566_1r19 | CTTCACRTTCCGTGTCTCspC^spC | 0 | 1074,1 | - | 1377,3 | 1417,4 | - | |
| 25 | 25 | HLAA_2567_1r19 | CTTCASITGCCGTGTCTCspC^spC | 0 | 1074,1 | - | 1377,3 | 1417,4 | - |
| 26 | HLAA_2568_1r19 | CTTCAGTTKCCGTGTCTCspC^spC | 0 | 1074,1 | - | 1377,3 | 1417,4 | - | |
| 28 | HLAA_2681_1f20 | ATTGGGACCGGAACACACspG^spG | 0 | 1154,1 | 1481,4 | 1457,3 | - | - | |
| 29 | HLAA_2682_1f20 | ATTGGGACCTGCAGACACspG^spG | 0 | 1154,1 | 1481,4 | 1457,3 | - | - | |
| 30 | HLAA_2683_1f20 | ATTGGGACSGGGAGACACspG^spG | 0 | 1154,1 | 1481,4 | 1457,3 | - | - | |
| 31 | HLAA_2684_1f20 | ATTGGGACSGGGAGACACspG^spG | 0 | 1154,1 | 1481,4 | 1457,3 | - | - | |
| 20 | 32 | HLAA_2685_1f20 | ATTGGGACSGGGAGACAGspG^spG | 0 | 1194,1 | 1521,4 | - | - | |
| 33 | HLAA_2701_1r19 | CTGTGAGTGGGCCCTCspA^spT | 0 | 1113,1 | 1440,4 | - | - | - | |
| 34 | HLAA_2702_1r19 | CTGTGACTGGGCCYTCspA^spC | -14 | 1084,1 | 1411,4 | - | 1427,4 | 1402,4 | |
| 35 | HLAA_2703_1r19 | CTGTGAGTGGSCCTTCspA^spC | -14 | 1084,1 | 1411,4 | - | 1427,4 | 1402,4 | |
| 36 | HLAA_2821_1f20 | ACACGGAAATGTGARGGCCspC^spA | 0 | 1098,1 | - | 1401,3 | 1441,3 | - | |
| 37 | HLAA_2822_1f20 | ACASGGAAAGTGAAGGCCspC^spA | 0 | 1098,1 | - | 1401,3 | 1441,3 | - | |
| 25 | 38 | HLAA_2823_1f20 | ACACGGCAWGTGAAGGCCspC^spA | 0 | 1098,1 | - | 1401,3 | 1441,3 | - |
| 39 | HLAA_2824_1f20 | ACACGGAAACGTGAAGGCCspC^spA | 0 | 1098,1 | - | 1401,3 | 1441,3 | - | |
| 40 | HLAA_2825_1f20 | ACACGGAAATRTGAAGGCCspC^spA | 0 | 1098,1 | - | 1401,3 | 1441,3 | - | |
| 41 | HLAA_2921_2f20 | TGAAGGCCCACTCACAGspAspG^spT | -14 | 1498,4 | - | 1801,6 | - | - | |
| 42 | HLAA_2922_2f20 | TGAAGGCCCACTCACAGspGspC^spT | 0 | 1488,4 | - | - | 1831,7 | - | |
| 43 | HLAA_2923_2f20 | TGAAGGCCCACTCACAGspAspT^spT | 0 | 1589,6 | - | - | 1932,9 | - | |
| 44 | HLAA_2924_2f20 | TGARGGCCAGTCACAGspAspC^spT | 0 | 1427,4 | - | 1775,6 | 1815,7 | - | |
| 45 | HLAA_2925_2f20 | TGAAGGCCCACTCACAGspAspC^spT | 0 | 1427,4 | - | 1775,6 | 1815,7 | - | |
| 30 | 46 | HLAA_3681_1f20 | TCACACCACATCCAGATAATspG^spC | 0 | 1129,1 | 1456,4 | - | - | |
| 47 | HLAA_3682_1f20 | TCACACCACATCCAGMTAATspG^spT | 0 | 1144,1 | 1471,6 | 1447,1 | 1487,4 | 1462,3 | |
| 48 | HLAA_3683_1f20 | TCACACCACATCCAGAGGATspG^spT | 0 | 1144,1 | 1471,6 | 1447,1 | 1487,4 | 1462,3 | |
| 49 | HLAA_3684_1f20 | TCACACCACATCCAGATGATspG^spT | 0 | 1144,1 | 1471,6 | 1447,1 | 1487,4 | 1462,3 | |
| 50 | HLAA_3961_2r20 | GCTGGTACCCGGAGspGspA^spG | 0 | 1537,4 | - | - | 1880,7 | - | |

| | | | | | | | | |
|-----|----------------|-----------------------------|-----|--------|--------|--------|--------|--------|
| 51 | HLAA_3962_2r20 | GCCGGTACCCGGAGGAGspTspA^spA | 0 | 1496,4 | - | - | 1839,7 | - |
| 52 | HLAA_3963_2r20 | GGTGGTACCCGYGCAGGspGspA^spA | 0 | 1496,4 | - | - | 1839,7 | - |
| 53 | HLAA_3964_2r20 | GGTGGTACCCGAGAGGspGspA^spA | 0 | 1521,5 | - | - | 1864,8 | 1839,7 |
| 54 | HLAA_3965_2r20 | GTTCATACCCGGAGGAGspGspA^spA | 0 | 1521,5 | - | - | 1864,8 | 1839,7 |
| 55 | HLAA_3966_2r20 | GSTGGTACCCGGAGGAGspGspA^spA | 0 | 1521,5 | - | - | 1864,8 | 1839,7 |
| 56 | HLAA_3967_2r20 | GCCGGTACCCGGAGGAGspGspA^spA | 0 | 1521,5 | - | - | 1864,8 | 1839,7 |
| | | | | | | | | |
| 57 | HLAA_4141_1f20 | CGCTTCCCTCGCGGGTATspG^spA | 0 | 1153,1 | 1480,1 | - | - | - |
| 58 | HLAA_4142_1f20 | CGCTTCCCTCGCGGGTACspC^spA | 0 | 1098,1 | - | 1401,3 | 1441,4 | - |
| 59 | HLAA_4143_1f20 | CGCTTCCCTCGCGGGTACspC^spA | 0 | 1098,1 | - | 1401,3 | 1441,4 | - |
| 60 | HLAA_4144_1f20 | CGCTTCCCTCACGGGTACspC^spA | 0 | 1098,1 | - | 1401,3 | 1441,4 | - |
| 61 | HLAA_4145_1f20 | CGMTTCCCTCGCGGGTACspC^spA | 0 | 1098,1 | - | 1401,3 | 1441,4 | - |
| 62 | HLAA_4146_1f20 | CGCTTCCCTCGCGGGTACspC^spA | 0 | 1098,1 | - | 1401,3 | 1441,4 | - |
| 63 | HLAA_4147_1f20 | CACTTCCCTCGCGGGTACspC^spG | 0 | 1114,1 | - | - | 1457,4 | - |
| 64 | HLAA_4148_1f20 | CGCTTMCCTCGCGGGTACspC^spG | 0 | 1114,1 | - | - | 1457,4 | - |
| | | | | | | | | |
| 65 | HLAA_4531_1r20 | GTCCAAGAGCGCAGGTCTspT^spC | 0 | 1206,2 | - | - | - | 1524,4 |
| 66 | HLAA_4532_1r20 | GTCCAAGAGCGCAGGTCCspT^spC | 0 | 1191,2 | - | - | 1534,5 | 1509,4 |
| 67 | HLAA_4533_1r20 | GTCCAGGAGCTCAGGTCCspT^spC | 0 | 1191,2 | - | - | 1534,5 | 1509,4 |
| | | | | | | | | |
| 68 | HLAA_5021_2r20 | GGCCGYCTCCCACTTGspGspC^spT | 0 | 1463,4 | - | - | - | 1781,6 |
| 69 | HLAA_5022_2r20 | GGCYGCCTCCCACTTGspGspC^spT | 0 | 1448,4 | - | 1751,6 | 1791,7 | 1766,6 |
| 70 | HLAA_5023_2r20 | CGGAGTCTCCCACTTGspGspC^spT | 0 | 1448,4 | - | 1751,6 | 1791,7 | 1766,6 |
| 71 | HLAA_5024_2r20 | GGCCGCCCTCCCACTTGspGspC^spC | -14 | 1419,4 | - | - | - | 1737,6 |
| | | | | | | | | |
| 72 | HLAA_5271_1f20 | AGTGGGAGACTCCGCCAspT^spG | 0 | 1255,3 | 1582,6 | 1558,5 | - | 1573,5 |
| 73 | HLAA_5272_1f20 | CAAGTGGAGGGGGYCCAspT^spG | 0 | 1255,3 | 1582,6 | 1558,5 | - | 1573,5 |
| 74 | HLAA_5273_1f20 | CAAGTGGAGRCGGCCCAspT^spG | 0 | 1255,3 | 1582,6 | 1558,5 | - | 1573,5 |
| 75 | HLAA_5274_1f20 | CAAGTGGAGGGGGCCAspT^spG | 0 | 1246,3 | - | - | - | 1564,5 |
| 76 | HLAA_5275_1f20 | CAAGTGGAGGGGGCCGspT^spT | 0 | 1246,3 | - | - | 1589,6 | - |
| 77 | HLAA_5276_1f20 | CAAGTGGAGGGGGCCGspT^spC | 0 | 1231,3 | - | - | 1574,5 | - |
| 78 | HLAA_5277_1f20 | CAAGTGGAGGGGGCCMGspT^spG | 0 | 1271,3 | 1598,6 | - | - | 1589,5 |
| 79 | HLAA_5278_1f20 | CAAGTGGAGGGCRGCCCAspT^spG | 0 | 1271,3 | 1598,6 | - | - | 1589,5 |
| | | | | | | | | |
| 80 | HLAA_5391_1f19 | GCCCRTGAGGGGGAGCAspG^spC | 0 | 1138,1 | 1465,4 | - | 1481,4 | 1456,3 |
| 81 | HLAA_5392_1f19 | GYCCATGCGGGGGAGCAspG^spC | 0 | 1138,1 | 1465,4 | - | 1481,4 | 1456,3 |
| 82 | HLAA_5393_1f19 | GCCCCTGCGGGGGAGCAspG^spC | 0 | 1138,1 | 1465,4 | - | 1481,4 | 1456,3 |
| 83 | HLAA_5394_1f19 | GCCCCTGTGGGGAGCAspG^spC | 0 | 1138,1 | 1465,4 | - | 1481,4 | 1456,3 |
| 84 | HLAA_5395_1f19 | GTCCATGCGGGGGAGCAspG^spT | 0 | 1153,1 | - | - | 1496,4 | 1471,3 |
| 85 | HLAA_5396_1f19 | GCCCCTYGGGGGGAGCAspG^spT | 0 | 1153,1 | - | - | 1496,4 | 1471,3 |
| 86 | HLAA_5397_1f19 | GCCCCATGAGGGGGAGCAspG^spT | 0 | 1153,1 | - | - | 1496,4 | 1471,3 |
| 87 | HLAA_5398_1f19 | GCCCWTGTGGGGAGCAspG^spT | 0 | 1153,1 | - | - | 1496,4 | 1471,3 |
| 88 | HLAA_5399_1f19 | GCCMGTGTGGGGAGCAspG^spT | 0 | 1153,1 | - | - | 1496,4 | 1471,3 |
| | | | | | | | | |
| 89 | HLAA_5591_1r20 | GCGGAGCCACTCCACGCAspC^spT | 0 | 1113,1 | - | 1416,3 | - | - |
| 90 | HLAA_5592_1r20 | GCGGAGCCCTCCACGCAspC^spT | 0 | 1113,1 | - | 1416,3 | - | - |
| 91 | HLAA_5593_1r20 | GCGGAGCCACTCCACGCAspC^spA | 0 | 1122,1 | - | - | 1465,4 | - |
| 92 | HLAA_5594_1r20 | GCGGAGCCCGTCCACTCAspC^spG | 0 | 1138,1 | - | - | - | 1456,3 |
| 93 | HLAA_5595_1r20 | GCGGAGCCAGTCCACGCAspC^spG | 0 | 1138,1 | - | - | - | 1456,3 |
| 94 | HLAA_5596_1r20 | GCGGAGCCMGTCCACGCAspC^spG | 0 | 1138,1 | - | - | - | 1456,3 |
| 95 | HLAA_5597_1r20 | GCGGAGCCACTCCACGCAspC^spC | 0 | 1098,1 | 1425,4 | - | 1441,4 | - |
| 96 | HLAA_5598_1r20 | GCGGAGCCCGTCCACGCAspC^spC | 0 | 1098,1 | 1425,4 | - | 1441,4 | - |
| 97 | HLAA_5599_1r20 | GCGGAGCCACTCCACGCAspG^spG | 0 | 1178,1 | - | - | - | 1496,3 |
| | | | | | | | | |
| 98 | HLAA_5711_2f20 | TGGAGGGCCCKTGCCTGspGspA^spG | 0 | 1537,4 | - | - | - | 1855,6 |
| 99 | HLAA_5712_2f20 | TGGAGGGYGAATGCCTGspGspA^spG | 0 | 1537,4 | - | - | - | 1855,6 |
| 100 | HLAA_5713_2f20 | TGSAGGGCCGGTGCCTGspGspA^spG | 0 | 1537,4 | - | - | - | 1855,6 |
| 101 | HLAA_5714_2f20 | TGGATGSCACGTGCGTGspGspA^spG | 0 | 1537,4 | - | - | - | 1855,6 |
| 102 | HLAA_5715_2f20 | TGGAGGGCACSTGCGTGspGspA^spG | 0 | 1537,4 | - | - | - | 1855,6 |
| 103 | HLAA_5716_2f20 | TGGAGGGCACGTGCGTGspGspA^spC | 0 | 1497,4 | - | - | 1840,7 | 1815,6 |
| 104 | HLAA_5717_2f20 | TGGAGGGCYGGTGCCTGspGspA^spC | 0 | 1497,4 | - | - | 1840,7 | 1815,6 |

TABLE V

| No | Name | Sequence | CT | Primer Masses | A | C | G | T |
|----|-----------------|------------------------------|-----|---------------|--------|--------|--------|--------|
| 1 | HLAB_971_2f20 | CCCACTCCATGAGGCATspTspT^spC | 0 | 1540,3 | - | 1843,7 | 1883,8 | 1858,7 |
| 2 | HLAB_972_2f20 | CCCACTYCATGAGGTATspTspT^spC | 0 | 1540,3 | - | 1843,7 | 1883,8 | 1858,7 |
| 3 | HLAB_2061_1f20 | CGACGCCGCGAGTCAGGAGGSpG^spA | -28 | 1150,1 | 1477,4 | 1453,3 | - | 1468,3 |
| 4 | HLAB_2062_1f20 | CGACGCCACGAGTCCGAGGSpG^spA | -28 | 1150,1 | 1477,4 | 1453,3 | - | 1468,3 |
| 5 | HLAB_2063_1f20 | CGACGCCGCGAGTCCRAGGSpA^spG | 0 | 1178,1 | 1505,4 | - | 1521,4 | - |
| 6 | HLAB_2064_1f20 | CGACGCCRCGAGTCCGAGGSpA^spG | 0 | 1178,1 | 1505,4 | - | 1521,4 | - |
| 7 | HLAB_2221_1r19 | GCCCCCTCCTGCTCCACCSpC^spA | 0 | 1098,3 | 1425,4 | - | 1441,4 | - |
| 8 | HLAB_2222_1r19 | GCCCCCTCYTGCTCTATCSpC^spA | 0 | 1098,3 | 1425,4 | - | 1441,4 | - |
| 9 | HLAB_2591_2f20 | GGCCGGAGTATTGGGACSpGSpG^spG | 0 | 1513,4 | - | - | 1856,7 | - |
| 10 | HLAB_2592_2f20 | GGCCGGAGTATTGGGACSpGSpA^spG | 0 | 1497,4 | - | - | 1840,7 | - |
| 11 | HLAB_2593_2f20 | GGCCGGAGTATTGGGACSpCSpC^spG | -28 | 1405,4 | - | - | 1748,7 | - |
| 12 | HLAB_2594_2f20 | GGCCGGAGTATTGGGATSpCSpG^spG | 0 | 1488,4 | 1815,7 | - | 1831,7 | - |
| 13 | HLAB_2595_2f20 | GGCCGGAGTTTGGGACSpCSpG^spG | -28 | 1445,4 | 1772,7 | - | 1788,7 | - |
| 14 | HLAB_2596_2f20 | GGCCGGAGCATTGGGACSpCSpG^spG | -28 | 1445,4 | 1772,7 | - | 1788,7 | - |
| 15 | HLAB_2597_2f20 | GGCCGGAGATTGGGACSpCSpG^spG | -28 | 1445,4 | 1772,7 | - | 1788,7 | - |
| 16 | HLAB_2598_2f20 | GGCCRGAATATTGGGACSpCSpG^spG | -28 | 1445,4 | 1772,7 | - | 1788,7 | - |
| 17 | HLAB_2599_2f20 | GGCGGGMGTATTGGGACSpCSpG^spG | -28 | 1445,4 | 1772,7 | - | 1788,7 | - |
| 18 | HLAB_25910_2f20 | GGCCTAGTATTGGGACSpCSpG^spG | -28 | 1445,4 | 1772,7 | - | 1788,7 | - |
| 19 | HLAB_2721_1f20 | GGACSGGGAGACACGGAAspC^spA | 0 | 1122,1 | - | - | - | 1440,3 |
| 20 | HLAB_2722_1f20 | GGACGRGGAGACACGGAAspC^spA | 0 | 1122,1 | - | - | - | 1440,3 |
| 21 | HLAB_2723_1f20 | GGACCGGAACACACAGAAspC^spT | 0 | 1113,1 | - | - | 1456,4 | - |
| 22 | HLAB_2724_1f20 | GGACCGGAACACACAGACSpC^spT | -14 | 1075,1 | - | - | - | 1393,3 |
| 23 | HLAB_2725_1f20 | GGACCGGGAGACACAGAAspC^spT | 0 | 1153,1 | 1480,4 | - | - | - |
| 24 | HLAB_2726_1f20 | GGACCGGGAGATACAGATSpC^spT | 0 | 1104,1 | 1431,4 | 1407,3 | 1447,4 | 1422,3 |
| 25 | HLAB_2727_1f20 | GGACCGGGASACACAGATSpC^spT | 0 | 1104,1 | 1431,4 | 1407,3 | 1447,4 | 1422,3 |
| 26 | HLAB_2728_1f20 | GGACCGGGACACACAGATSpC^spT | 0 | 1104,1 | 1431,4 | 1407,3 | 1447,4 | 1422,3 |
| 27 | HLAB_2729_1f20 | GGACCSGGAGACACAGATSpC^spT | 0 | 1104,1 | 1431,4 | 1407,3 | 1447,4 | 1422,3 |
| 28 | HLAB_2921_2f19 | CAAGACCAACACACAGSpGSpC^spT | 0 | 1458,3 | - | - | 1801,6 | - |
| 29 | HLAB_2922_2f19 | CAAGSCCCAGGCACAGSpGSpC^spT | 0 | 1458,3 | - | - | 1801,6 | - |
| 30 | HLAB_2923_2f19 | CAAGACCAACACACAGGSpAspC^spT | -28 | 1414,3 | - | - | 1757,6 | 1732,5 |
| 31 | HLAB_2924_2f19 | GAAGGCCTCCGCGAGSpAspC^spT | -28 | 1414,3 | - | - | 1757,6 | 1732,5 |
| 32 | HLAB_2925_2f19 | CAAGGCCMAGGCACAGSpAspC^spT | -28 | 1414,3 | - | - | 1757,6 | 1732,5 |
| 33 | HLAB_2926_2f19 | CAAGSGCCAGGCACAGSpAspC^spT | -28 | 1414,3 | - | - | 1757,6 | 1732,5 |
| 34 | HLAB_2927_2f19 | GAAGACCAACACACAGSpAspC^spT | -28 | 1414,3 | - | - | 1757,6 | 1732,5 |
| 35 | HLAB_3021_2f19 | GCACAGACTGACCGAGSpTspG^spG | 0 | 1528,4 | - | - | 1871,7 | - |
| 36 | HLAB_30211_2f19 | ACACAGACTTACAGAGSpAspG^spA | -28 | 1493,5 | 1820,8 | - | 1836,8 | - |
| 37 | HLAB_3022_2f19 | ACACAGACTTACCGAGSpAspG^spG | 0 | 1537,4 | 1864,7 | - | - | - |
| 38 | HLAB_3023_2f19 | RCACAGACTGACCGAGSpAspG^spG | 0 | 1537,4 | 1864,7 | - | - | - |
| 39 | HLAB_3024_2f19 | GCACAGACTGGCCGAGSpTspG^spA | -28 | 1481,4 | 1811,7 | - | 1827,7 | - |
| 40 | HLAB_3025_2f19 | ACACAGACTTACCGAGSpTspG^spA | -28 | 1481,4 | 1811,7 | - | 1827,7 | - |
| 41 | HLAB_3026_2f19 | RCACAGACTGACCGAGSpTspG^spA | -28 | 1481,4 | 1811,7 | - | 1827,7 | - |
| 42 | HLAB_3027_2f19 | ACACAGGCTGACCGAGSpAspG^spA | -28 | 1493,5 | 1820,8 | - | 1836,8 | - |
| 43 | HLAB_3028_2f19 | RCACAGACTGACCGAGSpAspG^spA | -28 | 1493,5 | 1820,8 | - | 1836,8 | - |
| 44 | HLAB_3029_2f19 | GCRCAGACTTACCGAGSpAspG^spA | -28 | 1493,5 | 1820,8 | - | 1836,8 | - |
| 45 | HLAB_30210_2f19 | ACACRGACTTACCGAGSpAspG^spA | -28 | 1493,5 | 1820,8 | - | 1836,8 | - |
| 46 | HLAB_3621_2f20 | CGGGTCTCACACCCCTCCSpAspC^spA | -28 | 1413,4 | - | - | 1756,7 | - |
| 47 | HLAB_3622_2f20 | CGGGTCTCACAYCATCCSpAspG^spA | -14 | 1467,4 | 1794,7 | 1770,6 | 1810,7 | 1785,6 |
| 48 | HLAB_3623_2f20 | CGGGTCTCACACCCCTCCSpAspG^spA | -14 | 1467,4 | 1794,7 | 1770,6 | 1810,7 | 1785,6 |
| 49 | HLAB_3624_2f20 | CGGGTCTCACACTTGGCSpAspG^spA | -14 | 1467,4 | 1794,7 | 1770,6 | 1810,7 | 1785,6 |
| 50 | HLAB_3625_2f20 | CGGGTCTCACATCATCCSpAspG^spG | -14 | 1483,4 | - | - | - | 1801,6 |
| 51 | HLAB_3626_2f20 | CGGGTCTCACACCCCTCCSpAspG^spT | 0 | 1472,4 | - | - | 1815,7 | - |
| 52 | HLAB_3631_1r20 | CCCASGTCGCAGCCGTACSpA^spT | -28 | 1085,1 | - | 1388,3 | 1428,4 | 1403,3 |
| 53 | HLAB_3632_1r20 | CCCAAGTCGCAGCCATACSpA^spT | -28 | 1085,1 | - | 1388,3 | 1428,4 | 1403,3 |
| 54 | HLAB_3633_1r20 | CCCASGTCGCAGCCAAACSpA^spT | -28 | 1085,1 | - | 1388,3 | 1428,4 | 1403,3 |

| | | | | | | | | |
|----|-----------------|------------------------------|-----|--------|--------|--------|--------|--------|
| 55 | HLAB_3634_1r20 | CCCACGTCGCAGGCCAGACSpA^spT | -28 | 1085,1 | - | 1388,3 | 1428,4 | 1403,3 |
| 56 | HLAB_3635_1r20 | CCCACGTCGCAGCCGACSpA^spT | -28 | 1085,1 | - | 1388,3 | 1428,4 | 1403,3 |
| 57 | HLAB_3636_1r20 | CCCACGTCGCAGCCCTACSpA^spT | -28 | 1085,1 | - | 1388,3 | 1428,4 | 1403,3 |
| 58 | HLAB_3637_1r20 | CCCACGTCGCAGCCGTACSpG^spT | 0 | 1129,1 | - | 1432,3 | 1472,4 | 1447,3 |
| | | | | | | | | |
| 59 | HLAB_3691_1f20 | TCCGGCCCCAKGTCGCAGSpC^spC | 0 | 1114,1 | 1441,4 | - | 1457,4 | 1432,3 |
| 60 | HLAB_3692_1f20 | TCGGGGCCCCASGTCGCAGSpC^spC | 0 | 1114,1 | 1441,4 | - | 1457,4 | 1432,3 |
| | | | | | | | | |
| 55 | HLAB_4121_2f20 | GGCGCCTCCTCCCGCGGGSpTSpA^spC | -28 | 1444,4 | - | 1747,6 | - | - |
| 56 | HLAB_4122_2f20 | GGCGCCTCCTCCSCGGGSpCSpA^spT | 0 | 1472,4 | 1799,7 | - | 1815,7 | - |
| 57 | HLAB_4123_2f20 | GGCGCYTCCTCCCGCGGGSpCSpA^spT | 0 | 1472,4 | 1799,7 | - | 1815,7 | - |
| 58 | HLAB_4124_2f20 | GGCGTCTCCTCCCGCGGTSpTSpA^spT | 0 | 1462,4 | - | 1765,6 | - | - |
| 59 | HLAB_4125_2f20 | GGCGCCTCCTCCCGCGGGSpTSpA^spT | -14 | 1473,4 | - | 1776,6 | - | - |
| | | | | | | | | |
| 60 | HLAB_4181_2f20 | TCCTCCGCGGGTATGAAspCSpA^spG | 0 | 1481,4 | 1808,7 | - | - | - |
| 61 | HLAB_4182_2f20 | TCCTCCACGGGTACCAcSpCSpA^spG | 0 | 1457,4 | - | - | - | 1775,6 |
| 62 | HLAB_4183_2f20 | TCCTGCGCGGGTACCAcSpCSpA^spG | 0 | 1457,4 | - | - | - | 1775,6 |
| 63 | HLAB_4184_2f20 | TCCTCCGCGGGTACCAcSpCSpA^spG | 0 | 1457,4 | - | - | - | 1775,6 |
| 64 | HLAB_4185_2f20 | TCCTCTGCGGGTACCAcSpCSpA^spG | 0 | 1457,4 | - | - | - | 1775,6 |
| 65 | HLAB_4186_2f20 | TCCTCCGCGGGTACCAAGSpCSpA^spG | 0 | 1497,4 | 1824,7 | 1800,6 | 1840,7 | 1815,6 |
| 66 | HLAB_4187_2f20 | TMCTCCGCGGGTACCGGSpCSpA^spG | 0 | 1497,4 | 1824,7 | 1800,6 | 1840,7 | 1815,6 |
| 67 | HLAB_4188_2f20 | TCCTCCGCGGGTACCAAGSpCSpG^spG | 0 | 1513,4 | - | - | 1856,7 | - |
| | | | | | | | | |
| 68 | HLAB_4191_2r20 | AATCCTTGCCTCGTAGSpGSpC^spT | -14 | 1474,4 | 1801,7 | - | - | - |
| 69 | HLAB_4192_2r20 | AATCCTTGCCTCGTAGSpGSpC^spA | -28 | 1469,4 | - | - | - | 1812,7 |
| 70 | HLAB_4193_2r20 | AATTCTGCCGTCTCGTAGSpGSpC^spG | 0 | 1513,4 | 1840,7 | - | 1856,7 | 1831,6 |
| 71 | HLAB_4194_2r20 | AATCTTGCCGTCTCGTAGSpGSpC^spG | 0 | 1513,4 | 1840,7 | - | 1856,7 | 1831,6 |
| 72 | HLAB_4195_2r20 | AATCCTTGCCTCGYAGSpGSpC^spG | 0 | 1513,4 | 1840,7 | - | 1856,7 | 1831,6 |
| | | | | | | | | |
| 73 | HLAB_4351n_1r20 | TCMTTCAGGGCGATGTAAspT^spC | -14 | 1201,3 | - | 1504,4 | - | 1519,4 |
| 74 | HLAB_4352n_1r20 | TCGTTTCAGGGCGATGTAAspT^spT | 0 | 1230,3 | - | 1533,5 | - | - |
| | | | | | | | | |
| 75 | HLAB_5271_1f20 | CAAGTGGAGGCAGGCCCTSpT^spG | 0 | 1246,3 | - | - | - | 1564,5 |
| 76 | HLAB_5272_1f20 | CAAGTKGGAGGCAGGCCGSpT^spG | 0 | 1271,3 | 1598,6 | 1574,3 | - | 1589,5 |
| | | | | | | | | |
| 77 | HLAB_5391_1f20 | GGCCCGTGYGGCGGGAGCAspC^spC | 0 | 1138,1 | - | - | 1481,3 | 1456,3 |
| 78 | HLAB_5392_1f20 | GGCCCGTGTGCGGGAGCAspC^spG | 0 | 1178,1 | 1505,4 | - | - | - |
| 79 | HLAB_5393_1f20 | GGCCCGTGWGGCGGAGCAspC^spG | 0 | 1178,1 | 1505,4 | - | - | - |
| 80 | HLAB_5394_1f20 | GGCCCGTGAAGCGGGAGCAspC^spT | 0 | 1153,1 | - | - | 1496,4 | - |
| | | | | | | | | |
| 81 | HLAB_5591_1r20 | GCGGAGCGACTCCACGCAspC^spT | 0 | 1113,1 | - | - | 1456,4 | - |
| 82 | HLAB_5592_1r20 | GCGGAGCCACTCCACGCAspC^spT | 0 | 1113,1 | - | - | 1456,4 | - |
| 83 | HLAB_5593_1r20 | GCGGAGCCAATCCACGCAspC^spT | 0 | 1113,1 | - | - | 1456,4 | - |
| 84 | HLAB_5594_1r20 | GCGGAGCCACTCCACGCAspC^spG | 0 | 1152,1 | - | - | - | 1470,3 |
| 85 | HLAB_5595_1r20 | GCGGAGCGACTCCRCGCAspC^spA | -14 | 1122,1 | 1449,1 | 1425,3 | - | - |
| 86 | HLAB_5596_1r20 | GCGGAGCSACTCCACGCAspC^spA | -14 | 1122,1 | 1449,1 | 1425,3 | - | - |
| 87 | HLAB_5597_1r20 | GCGGAGCCCCGTCACGCAspC^spA | -14 | 1122,1 | 1449,1 | 1425,3 | - | - |
| | | | | | | | | |
| 88 | HLAB_5711_1r20 | CTCCAGGTAYCTGCAGGSpC^spG | 0 | 1154,1 | 1481,4 | - | - | - |
| 89 | HLAB_5712_1r20 | CTCCAGGTRCTGCAGGSpC^spC | 0 | 1114,1 | 1441,4 | 1417,3 | - | - |
| | | | | | | | | |
| 90 | HLAB_583_1r19 | ACCTGGAGAACGGGAAGSpGSpA | 0 | 1178,1 | 1505,4 | - | 1521,4 | - |

20
TABLE VI

| No | Name | Sequence | CT | Masses | | | |
|----|----------------|----------------------------|-----|--------|--------|--------|--------|
| | | | | Primer | A | C | G |
| | | | | | | | T |
| 1 | DRB1_1251_1r20 | CATTGAAGAAATGACACTspC^spC | 0 | 1098,1 | - | 1392,3 | - |
| 2 | DRB1_1252_1r20 | CGTTGAAGAAATGACACTspT^spA | 0 | 1230,1 | - | - | 1548,5 |
| 3 | DRB1_1253_1r20 | CATTGAAGAAATGACATTspC^spA | 0 | 1113,1 | 1440,4 | 1416,3 | 1456,4 |
| 4 | DRB1_1254_1r20 | CATTGAAGAAATGACACTspC^spA | 0 | 1113,2 | 1440,4 | 1416,3 | 1456,4 |
| 5 | DRB1_1255_1r20 | CGTTGAAGAAATGACACTspC^spA | 0 | 1113,3 | 1440,4 | 1416,3 | 1456,4 |
| 6 | DRB1_1961_1f19 | CATCTATAACCAAGAGGspA^spA | 0 | 1162,1 | - | - | 1480,3 |
| 7 | DRB1_1962_1f19 | CTTCTATCACCAAGARGspA^spG | 0 | 1178,1 | 1505,4 | - | 1496,3 |
| 8 | DRB1_1963_1f19 | CTTCTATAATCARGAGGspA^spG | 0 | 1178,1 | 1505,4 | - | 1496,3 |
| 9 | DRB1_1964_1f19 | CGTCCATAACCAAGAGGspA^spG | 0 | 1178,1 | 1505,4 | - | 1496,3 |
| 10 | DRB1_1965_1f19 | CATCTATAACCAAGAGGspA^spG | 0 | 1178,1 | 1505,4 | - | 1496,3 |
| 11 | DRB1_1966_1f19 | CTTCCATAACCRGGAGGspA^spG | 0 | 1178,1 | 1505,4 | - | 1496,3 |
| 12 | DRB1_1967_1f19 | CTTCGATAACCAGGAGGspA^spG | 0 | 1178,1 | 1505,4 | - | 1496,3 |
| 13 | DRB1_1968_1f19 | CTTCTATAACCTGGAGGspA^spG | 0 | 1178,1 | 1505,4 | - | 1496,3 |
| 14 | DRB1_1971_1r20 | CGTCGCTGTCGAAGCGCAspG^spG | 0 | 1178,1 | 1505,4 | - | 1496,3 |
| 15 | DRB1_1972_1r20 | CGTCGCTGTCGTAGCGCGspC^spG | 0 | 1154,1 | - | - | 1472,3 |
| 16 | DRB1_1973_1r20 | CGTCGCTGTCGAAGCGCAspA^spG | 0 | 1162,1 | - | - | 1480,3 |
| 17 | DRB1_1974_1r20 | CGTCGCTGTCGAAGYGCAspC^spG | -28 | 1110,1 | 1437,4 | - | 1453,4 |
| 18 | DRB1_1975_1r20 | CGTCGCTGTCGAASCGCCAspC^spG | -28 | 1110,1 | 1437,4 | - | 1453,4 |
| 19 | DRB1_2271_1f20 | CGACAGCGACGTGGGGGAspC^spT | 0 | 1113,1 | 1440,4 | - | - |
| 20 | DRB1_2272_1f20 | CGACAGCGACGTGVGGGAspG^spT | 0 | 1153,1 | 1480,4 | - | 1471,3 |
| 21 | DRB1_2611_1r20 | TTCTGGCTGTTCCAGTACspT^spG | 0 | 1231,2 | - | - | 1574,5 |
| 22 | DRB1_2612_1r20 | TTCTGGCTGTTCCAGTACspC^spC | 0 | 1074,1 | - | 1377,3 | - |
| 23 | DRB1_2613_1r20 | TTCTGGCTGTTCCAGTAGspT^spC | 0 | 1231,2 | - | 1534,4 | - |
| 24 | DRB1_2614_1r20 | TTCTGGCTGTTCCAGTRCspT^spC | -14 | 1177,2 | 1504,5 | 1480,4 | 1520,5 |
| 25 | DRB1_2615_1r20 | TTCYGGCTGTTCCAGGACspT^spC | -14 | 1177,2 | 1504,5 | 1480,4 | 1520,5 |
| 26 | DRB1_2861_1f19 | CTGGAACAGCCAGAAGAspA^spC | -28 | 1122,1 | 1449,4 | - | - |
| 27 | DRB1_2862_1f19 | CTGGAACAGCCRGAAAGGspA^spC | 0 | 1138,1 | 1465,4 | 1441,3 | - |
| 28 | DRB1_2991_1f20 | GAAGGACHTCCTGGAGCAspG^spG | 0 | 1178,1 | - | 1481,3 | - |
| 29 | DRB1_2992_1f20 | GAAGGACATCCTGGGAGAspC^spA | -14 | 1108,1 | 1435,1 | - | 1451,4 |
| 30 | DRB1_2993_1f20 | GAAGGACATCCTGGARGAspC^spA | -14 | 1108,1 | 1435,1 | - | 1452,4 |
| 31 | DRB1_2994_1f20 | GAAGGACYTCTGGAGAspC^spA | -14 | 1108,1 | 1435,1 | - | 1453,4 |
| 32 | DRB1_2995_1f20 | GAAGGACATCCTGGAGCAspG^spA | 0 | 1162,1 | 1489,4 | - | 1505,4 |
| 33 | DRB1_2996_1f20 | GAAGGACHTCCTGGAGCGspG^spA | 0 | 1178,1 | - | - | 1521,4 |
| 34 | DRB1_2997_1f20 | GAAGGACHTCCTGGAGAspC^spG | 0 | 1138,1 | 1465,4 | - | - |
| 35 | DRB1_3081_1r20 | GTCTGCAATAGGTGTCCAspC^spG | 0 | 1138,1 | - | 1441,3 | - |
| 36 | DRB1_3082_1r20 | GTCTGCARTAGGCGTCCAspC^spC | -14 | 1084,1 | 1411,4 | 1387,3 | 1427,4 |
| 37 | DRB1_3083_1r20 | GTCTGCAGTAATTGTCCAspC^spC | -14 | 1084,1 | 1411,4 | 1387,3 | 1427,4 |
| 38 | DRB1_3084_1r20 | GTCTGCACACGGTGTCCAspC^spC | -14 | 1084,1 | 1411,4 | 1387,3 | 1427,4 |
| 39 | DRB1_3085_1r20 | GTCTGCAGTAGGTGTCCAspC^spC | -14 | 1084,1 | 1411,4 | 1387,3 | 1427,4 |
| 40 | DRB1_3086_1r20 | GTCTGCAATAGGTGTCCAspC^spC | -14 | 1084,1 | 1411,4 | 1387,3 | 1427,4 |
| 41 | DRB1_341_1f19 | TGCAGACACAACSGspG^spG | 0 | 1194,1 | - | 1497,3 | - |
| 42 | DRB1_3451_1r20 | CGCTGCACTGTGAATCTCspT^spC | 0 | 1191,3 | 1518,5 | 1494,4 | - |
| 43 | DRB1_3452_1r20 | CTCTGCACTGTGAAGCTCspT^spC | 0 | 1191,3 | 1518,5 | 1494,4 | - |
| 44 | DRB1_3453_1r20 | CGCTGCACYGTGAAGCTCspT^spC | 0 | 1191,3 | 1518,5 | 1494,4 | - |

The resolution achievable by 19 markers each for HLA-A and HLA-B and the ten markers for HLA-DRB1 are listed in Tables VII to IX below.

TABLE VII

| Frequent Alleles of HLA-A | Group of frequent Alleles with same four-digit type | Rare Alleles with same Mini-Haplotype Profile | Resolution (in %) |
|---------------------------|--|---|-------------------|
| A*0101 | A*010101, A*010102 | A*0103, A*0104N, A*0109 | 98,3 |
| A*0201 | A*02010101, A*02010102N, A*020103, A*020104, A*020108, A*020109 | A*0204, A*0209, A*0225, A*0231, A*0232N, A*0242, A*0243N, A*0253N, A*0258, A*0260, A*0264, A*0266, A*0267 | 93,4 |
| | A*020102 | | 100 |
| | A*020105 | | 100 |
| | A*020106 | | 100 |
| | A*020107 | | 100 |
| A*0301 | A*03010101, A*03010102N | A*0303N, A*0304, A*0305, A*0306, A*0311N | 97,6 |
| | A*030102 | | 100 |
| | A*030103 | | 100 |
| A*2301 | A*2301 | A*2306, A*2307N, A*2308N | 98,6 |
| A*2402 | A*24020101, A*24020102N, A*240202, A*240203, A*240204 | A*2404, A*2409N, A*2411N, A*2426, A*2427, A*2432, A*2435, A*2436N, A*2437, A*2439 | 94,5 |
| A*2902 | A*290201 | A*29010101, A*29010102N, A*2906, A*2908N | 98,3 |
| | A*290202 | | 100 |
| A*3001 | A*3001 | | 100 |
| A*3002 | A*3002 | | 100 |

5

Capture: Alleles in a same field have the same mini-haplotype profile; grey highlighted are all alleles with identical sequences over exons 2 and 3.

TABLE VIII

| Frequent Alleles of HLA-B | Groups of frequent Alleles with same four-digit type | Rare Alleles with same Mini-Haplotype Profile | Resolution (in %) |
|---------------------------|--|---|-------------------|
| B*0702 | B*070201, B*070202, B*070203, B*070204 | B*0703, B*0721, B*0722, B*0723, B*0730, B*0733, B*0735 | 98,0 |
| B*0801 | B*0801 | B*0808N, B*0818, B*0819N | 99,3 |
| B*1302 | B*1302 | B*1308 | 99,6 |
| B*1501 | B*150101, B*150102N, B*150103, B*150104 | B*1528, B*1533, B*1534, B*1560, B*1575, B*1578, B*1579N, B*1581, B*1582 | 97,6 |
| | B*150102 | | 100 |
| B*1801 | B*180101, B*180102 | B*1805, B*1817N | 99,3 |
| B*3501 | B*350101, B*350102 | B*3507, B*3540N, B*3541, B*3542, B*5305 | 98,7 |
| B*3503 | B*3503 | B*3536 | 99,6 |
| B*4001 | B*400101, B*400102 | B*4011, B*401401, B*401402, B*401403, B*4022N | 98,7 |
| | B*400103 | | 100 |
| | B*400104 | B*4004 | 99,6 |
| B*4402 | B*44020101, B*44020102S, B*440202, B*440203 | B*4411, B*4419N, B*4422, B*4423N, B*4427, B*4433, B*4434, B*4435 | 97,8 |
| B*4403 | B*440301 | B*4413, B*4426, B*4429, B*4430, B*4432, B*4436, B*4437, B*4438, B*4439 | 98,2 |
| | B*440302 | B*4407 | 99,6 |
| B*5101 | B*510101, B*510102, B*510105 | B*5111N, B*5112, B*5114, B*5118, B*5126, B*5127N, B*5128, B*5130, B*5132, B*5133 | 97,6 |
| | B*510103 | | 100 |
| | B*510104 | B*5124 | 99,6 |
| B*5701 | B*570101 | B*5706, B*5708 | 99,5 |
| | B*570102 | | 100 |

Capture: Alleles in a same field have the same mini-haplotype profile; grey highlighted are all alleles with identical sequences over exons 2 and 3.

TABLE IX

| Frequent Alleles of HLA-DRB1* | Groups of frequent Alleles with same four-digit type | Rare Alleles with same Mini-Haplotype Profile | Resolution (in %) |
|-------------------------------|---|--|-------------------|
| DRB1*0101 | DRB1*010101 | DRB1*0105, DRB1*0107, DRB1*0111 | 98,9 |
| | DRB1*010102 | | 100 |
| DRB1*0301 | DRB1*030101, DRB1*030102 | DRB1*0307, DRB1*0312, DRB1*0313, DRB1*0315, DRB1*0316, DRB1*0318, DRB1*0322, DRB1*0323 | 97,2 |
| DRB1*0401 | DRB1*040101, DRB1*040102 | DRB1*0409, DRB1*0426, DRB1*0433 | 98,6 |
| DRB1*0701 | DRB1*070101, DRB1*070102 | DRB1*0703, DRB1*0704, DRB1*0705, DRB1*0707 | 98,3 |
| DRB1*1101 | DRB1*110101, DRB1*110102, DRB1*110103, DRB1*110104, DRB1*110105 | DRB1*112701, DRB1*112702, DRB1*1130, DRB1*1139 | 97,5 |
| DRB1*1104 | DRB1*110401, DRB1*110402 | DRB1*1134, DRB1*1146 | 98,9 |
| DRB1*1302 | DRB1*130201, DRB1*130202 | DRB1*1331, DRB1*1339, DRB1*1341 | 98,6 |
| DRB1*1501 | DRB1*150101, DRB1*150103, DRB1*150105 | DRB1*1503, DRB1*1506, DRB1*1509, DRB1*1513 | 98,0 |
| | DRB1*150102 | | 100 |
| | DRB1*150104 | DRB1*1512 | 99,4 |

Capture: Alleles in a same field have the same mini-haplotype profile; grey highlighted are all alleles with identical sequences over exon 2 (base 101 to 356)

5 The complete list of HLA alleles and sub-groups generated by the most informative mini-haplotyping markers (ten each for HLA-A, HLA-B and HLA-DRB1) are listed in Tables X to XII below.

TABLE X

TABLE XI

| | | | | | | | | | | |
|----------|---------|-----------|---------|-----------|---------|-----------|-----------|---------|-------------|---------|
| B-5307 | A G C T | T C G C C | C T G T | G T A T A | T C T T | C A G A G | G A G A A | G A T G | G G A C | G T C T |
| B-3503 | A G C T | T C G C C | C T G T | G C A T G | T C T T | C A G A G | G A G A A | G A T G | G G A C | G T A T |
| B-3513 | A G C T | T C G C C | C T G T | G C A T G | T C T T | C A G A G | G A G A A | G A T G | G G A C | G T A T |
| B-3536 | A G C T | T C G C C | C T G T | G C A T G | T C T T | C A G A G | G A G A A | G A T G | G G A C | G T A T |
| B-5304 | A G C T | T C G C C | C T G T | G C A T G | T C T T | C A G A G | G A G A A | G A T G | G G A C | G T A T |
| B-5611 | A G C T | T C G C C | C T G T | G C A T G | T C T A | C A G A G | G A G A A | G A T G | G A G A G | T A T |
| B-3533 | A G C T | T C G C C | G A G T | G C A T G | T C T T | C A G A G | G A G A A | G A T G | G G A C | G T A T |
| 5 B-4036 | A G C T | T C G C C | G A G T | G C A T A | T C T C | C A G A G | G A G A G | G A T G | G G A A G | T A C |
| B-4807 | A G C T | T C G C C | G A G T | G C A T A | T C T C | C A G A G | G A G A G | C A T G | G A G A G | T A C |
| B-7301 | A G C T | T C G C C | G A G T | G T A T A | T C T G | C A G A C | G T G G G | G A T G | G G A G A G | T A T |

10

15

20

25

30

TABLE XII

| Position in cDNA | 1 1 1 1 | 1 1 1 1 | 1 1 1 2 | 2 2 2 2 | 2 2 2 2 | 2 2 2 2 | 2 2 2 2 | 3 3 3 3 | 3 3 3 3 | 3 3 3 3 |
|------------------|-------------|-------------------------|---|---------|---------|---------|---------|---------|---------|---------|
| | 2 2 2 2 | 9 9 9 9 | 9 9 9 0 | 2 2 2 2 | 6 6 6 8 | 8 8 8 9 | 9 9 9 9 | 0 0 1 1 | 3 3 4 4 | 4 4 4 4 |
| | 5 6 7 8 | 3 4 5 6 | 7 8 9 0 | 4 5 6 7 | 1 2 3 4 | 3 4 5 6 | 6 7 8 9 | 8 9 0 1 | 8 9 0 1 | 2 3 4 5 |
| 5 | DRB1-070101 | A T A A G A G T T C G T | A G T A C G A G G A C A A C A G A G G T G G G T T G G T | | | | | | | |
| | DRB1-070102 | A T A A G A G T T C G T | A G T A C G A G G A C A A C A G A G G T G G G T T G G T | | | | | | | |
| | DRB1-0703 | A T A A G A G T T C G T | A G T A C G A G G A C A A C A G A G G T G G G T T G G T | | | | | | | |
| | DRB1-0704 | A T A A G A G T T C G T | A G T A C G A G G A C A A C A G A G G T G G G T T G G T | | | | | | | |
| | DRB1-0705 | A T A A G A G T T C G T | A G T A C G A G G A C A A C A G A G G T G G G T T G G T | | | | | | | |
| | DRB1-0707 | A T A A G A G T T C G T | A G T A C G A G G A C A A C A G A G G T G G G T T G G T | | | | | | | |
| | DRB1-0706 | A T A A G A G T T C G T | A G T A C G A G G A C A A C A G A G G T G G G T T G G T | | | | | | | |
| | DRB1-0708 | A T A A G A G G T C G T | A G T A C G A G G A C A A C A G A G G T G G G T T G G T | | | | | | | |
| 10 | DRB1-0441 | A T G A G A G A A C G T | A G T A C G A G G A C C A G A G A G G T G G G T T G T G | | | | | | | |
| | DRB1-0439 | A T G A G A G T A C G T | A C T A C G A G G A C C A G A G A G G T G G G T T G T G | | | | | | | |
| | DRB1-0416 | A T G A G A G T A C G T | A G T A C C A G G A C C A G A A C G G T G G G T T G G T | | | | | | | |
| | DRB1-0402 | A T G A G A G T A C G T | A G T A C G A G G A C A A C G A C G G T G G G T T G T G | | | | | | | |
| | DRB1-0412 | A T G A G A G T A C G T | A G T A C G A G G A C A A C A G T G G T G G G T T G T G | | | | | | | |
| | DRB1-0418 | A T G A G A G T A C G T | A G T A C G A G G A C A A C A G T G G T G G G T T G T G | | | | | | | |
| | DRB1-0414 | A T G A G A G T A C G T | A G T A C G A G G A C A A C G A C G G T G G G T T G G T | | | | | | | |
| 15 | DRB1-0438 | A T G A G A G T A C G T | A G T A C G A G G A C A A G A A C G G T G G G T T G G T | | | | | | | |
| | DRB1-0413 | A T G A G A G T A C G T | A G T A C G A G G A C C A G A A C G G T G G G T T G T G | | | | | | | |
| | DRB1-0422 | A T G A G A G T A C G T | A G T A C G A G G A C C A G A A G G G T G G G T T G T G | | | | | | | |
| 20 | DRB1-040101 | A T G A G A G T A C G T | A G T A C G A G G A C C A G A A C G G T G G G T T G G T | | | | | | | |
| | DRB1-040102 | A T G A G A G T A C G T | A G T A C G A G G A C C A G A A C G G T G G G T T G G T | | | | | | | |
| | DRB1-0409 | A T G A G A G T A C G T | A G T A C G A G G A C C A G A A C G G T G G G T T G G T | | | | | | | |
| | DRB1-0426 | A T G A G A G T A C G T | A G T A C G A G G A C C A G A A C G G T G G G T T G G T | | | | | | | |
| | DRB1-0433 | A T G A G A G T A C G T | A G T A C G A G G A C C A G A A C G G T G G G T T G G T | | | | | | | |
| | DRB1-0437 | A T G A G A G T A C G T | A G T A C G A G G A C C A C G A C G G T G G G T T G T G | | | | | | | |
| | DRB1-040301 | A T G A G A G T A C G T | A G T A C G A G G A C C A G A G A G G T G G G T T G T G | | | | | | | |
| | DRB1-0411 | A T G A G A G T A C G T | A G T A C G A G G A C C A G A G A G G T G G G T T G T G | | | | | | | |
| | DRB1-0427 | A T G A G A G T A C G T | A G T A C G A G G A C C A G A G A G G T G G G T T G T G | | | | | | | |
| 25 | DRB1-040701 | A T G A G A G T A C G T | A G T A C G A G G A C C A G A G A G G T G G G T T G G T | | | | | | | |
| | DRB1-040702 | A T G A G A G T A C G T | A G T A C G A G G A C C A G A G A G G T G G G T T G G T | | | | | | | |
| | DRB1-040703 | A T G A G A G T A C G T | A G T A C G A G G A C C A G A G A G G T G G G T T G G T | | | | | | | |
| | DRB1-0417 | A T G A G A G T A C G T | A G T A C G A G G A C C A G A G A G G T G G G T T G G T | | | | | | | |
| | DRB1-0404 | A T G A G A G T A C G T | A G T A C G A G G A C C A G A G C G G T G G G T T G T G | | | | | | | |
| | DRB1-0410 | A T G A G A G T A C G T | A G T A C G A G G A C C A G A G C G G T G G G T T G T G | | | | | | | |
| | DRB1-0423 | A T G A G A G T A C G T | A G T A C G A G G A C C A G A G C G G T G G G T T G T G | | | | | | | |
| | DRB1-0432 | A T G A G A G T A C G T | A G T A C G A G G A C C A G A G C G G T G G G T T G T G | | | | | | | |
| | DRB1-0440 | A T G A G A G T A C G T | A G T A C G A G G A C C A G A G C G G T G G G T T G T G | | | | | | | |
| | DRB1-0444 | A T G A G A G T A C G T | A G T A C G A G G A C C A G A G C G G T G G G T T G T G | | | | | | | |
| 30 | DRB1-040501 | A T G A G A G T A C G T | A G T A C G A G G A C C A G A G C G G T G G G T T G G T | | | | | | | |
| | DRB1-040502 | A T G A G A G T A C G T | A G T A C G A G G A C C A G A G C G G T G G G T T G G T | | | | | | | |
| | DRB1-040503 | A T G A G A G T A C G T | A G T A C G A G G A C C A G A G C G G T G G G T T G G T | | | | | | | |
| | DRB1-040504 | A T G A G A G T A C G T | A G T A C G A G G A C C A G A G C G G T G G G T T G G T | | | | | | | |
| | DRB1-0408 | A T G A G A G T A C G T | A G T A C G A G G A C C A G A G C G G T G G G T T G G T | | | | | | | |

| | |
|----------------|---|
| DRB1-0429 | ATGAGAGTACGTAGTACGAGGACCAAGAGCGGTTGGT |
| DRB1-0430 | ATGAGAGTACGTAGTACGAGGACCAAGAGCGGTTGGT |
| DRB1-0445 | ATGAGAGTACGTAGTACGAGGACCAAGAGCGGTTGGT |
| DRB1-0448 | ATGAGAGTACGTAGTACGAGGACCAAGAGCGGTTGGT |
| DRB1-0431 | ATGAGAGTACGTAGTACGAGGACCAAGAGCGGTTGGT |
| DRB1-0424 | ATGAGAGTACGTAGTACGAGGACCGGAGCGGTTGGT |
| 5 DRB1-0425 | ATGAGAGTACGTAGTACGAGGACTACAGTGGTGGGTTGGT |
| DRB1-0436 | ATGAGAGTACGTAGTACGAGGACTACAGCGGTTGGT |
| DRB1-0447 | ATGAGAGTACGTAGTACGAGGACACAGCGGTTGGT |
| DRB1-0415 | ATGAGAGTACGTAGTACGAGGACACAGCGGTTGGT |
| 10 DRB1-040302 | ATGAGAGTACGTAGTACGAGGACAGAGAGGTTGGTTGTG |
| DRB1-0435 | ATGAGAGTACGTAGTACGAGGACAGAGAGGTTGGTTGGT |
| DRB1-0442 | ATGAGAGTACGTAGTACGAGGACAGAGAGGTTGGTTGTG |
| DRB1-0428 | ATGAGAGTACGTAGTACGAGGACAGAGAGGTTGGTTGGT |
| DRB1-0443 | ATGAGAGTACGTAGTACGAGGACAGAGAGGTTGGTTGGT |
| 15 DRB1-1122 | ATGAGAGTACGTAGTACGAGGACAGAGAGGTTGGTTGTG |
| DRB1-0406 | ATGAGAGTACGTAGTACGAGGACAGAGAGGTTGGTTGTG |
| DRB1-0446 | ATGAGAGTACGTAGTACGAGGACAGAGAGGTTGGTTGTG |
| DRB1-0420 | ATGAGAGTACGTAGTACGAGGACAGAGAGGTTGGTTGTG |
| DRB1-0421 | ATGAGAGTACGTAGTACGAGGACAGAGAGGTTGGTTGTG |
| DRB1-0419 | ATGAGAGTACGTAGTACGAGGACAGAGAGGTTGGTTGTG |
| DRB1-1410 | ATGAGAGTACGTAGTACGAGGACAGAGAGGTTGGTTGTG |
| 20 DRB1-1332 | CTGAGAGAACGTAGTACGAGGACAAACGAGGGTTGGTTGTG |
| DRB1-1340 | CTGAGAGAACGTAGTACGAGGACAAACGAGGGTTGGTTGTG |
| DRB1-1353 | CTGAGAGAACGTAGTACGAGGACAAACGAGGGTTGGTTGTG |
| DRB1-1336 | CTGAGAGAACGTAGTACGAGGACAAACGAGGGTTGGTTGGT |
| DRB1-1424 | CTGAGAGAACGTAGTACGAGGACAAAGGCGGGTTGGTTGGT |
| DRB1-030201 | CTGAGAGAACGTAGTACGAGGACAGAAGGGTTGGTTGGT |
| 25 DRB1-030202 | CTGAGAGAACGTAGTACGAGGACAGAAGGGTTGGTTGGT |
| DRB1-0303 | CTGAGAGAACGTAGTACGAGGACAGAAGGGTTGGTTGTG |
| DRB1-0306 | CTGAGAGAACGTAGTACGAGGACAGAAGGGTTGGTTGTG |
| DRB1-1419 | CTGAGAGAACGTAGTACGAGGACAGAACGGTTGGTTGGT |
| DRB1-1429 | CTGAGAGAACGTAGTACGAGGACAGAGCGGTTGGCTGTG |
| DRB1-1406 | CTGAGAGAACGTAGTACGAGGACAGAGCGGTTGGTTGTG |
| 30 DRB1-1402 | CTGAGAGAACGTAGTACGAGGACAGAGCGGTTGGTTGTG |
| DRB1-1409 | CTGAGAGAACGTAGTACGAGGACAGAGCGGTTGGTTGTG |
| DRB1-1413 | CTGAGAGAACGTAGTACGAGGACAGAGCGGTTGGTTGTG |
| DRB1-1446 | CTGAGAGAACGTAGTACGAGGACAGAGCGGTTGGTTGTG |
| DRB1-1447 | CTGAGAGAACGTAGTACGAGGACAGAGCGGTTGGTTGTG |
| DRB1-1448 | CTGAGAGAACGTAGTACGAGGACAGAGCGGTTGGTTGTG |

| | | | |
|----|-------------|--------------|--------------------------------|
| | DRB1-1403 | CTGAGAGAACGT | AGTACGAGGGACCACAGTGGTGGGTTGGT |
| | DRB1-140302 | CTGAGAGAACGT | AGTACGAGGGACCACAGTGGTGGGTTGGT |
| | DRB1-1412 | CTGAGAGAACGT | AGTACGAGGGACCACAGTGGTGGGTTGGT |
| | DRB1-1418 | CTGAGAGAACGT | AGTATGAGGGACCGGAGGGTGGGTTGGT |
| 5 | DRB1-1326 | CTGAGAGAACGT | AGTATGAGGGACTACAGCGGTGGGTTGGT |
| | DRB1-1427 | CTGAGAGAACGT | AGTACGAGGGACTACAGGGTGGGTTGGT |
| | DRB1-1334 | CTGAGAGAACCT | AGTTCGAGGACAACGACGGTGGGTTGGT |
| | DRB1-0319 | CTGAGAGAACGT | AGTTCGAGGACAAGAAGGGTGGGTTGGT |
| | DRB1-1310 | CTGAGAGAACGT | AGTTCGAGGACAACAAACGGTGGGTTGGT |
| 10 | DRB1-130101 | CTGAGAGAACGT | AGTTCGAGGACAACGACGGTGGGTTGGT |
| | DRB1-130102 | CTGAGAGAACGT | AGTTCGAGGACAACGACGGTGGGTTGGT |
| | DRB1-130103 | CTGAGAGAACGT | AGTTCGAGGACAACGACGGTGGGTTGGT |
| | DRB1-1315 | CTGAGAGAACGT | AGTTCGAGGACAACGACGGTGGGTTGGT |
| | DRB1-1327 | CTGAGAGAACGT | AGTTCGAGGACAACGACGGTGGGTTGGT |
| | DRB1-1328 | CTGAGAGAACGT | AGTTCGAGGACAACGACGGTGGGTTGGT |
| | DRB1-1335 | CTGAGAGAACGT | AGTTCGAGGACAACGACGGTGGGTTGGT |
| | DRB1-1351 | CTGAGAGAACGT | AGTTCGAGGACAACGACGGTGGGTTGGT |
| | DRB1-1359 | CTGAGAGAACGT | AGTTCGAGGACAACGACGGTGGGTTGGT |
| | DRB1-1361 | CTGAGAGAACGT | AGTTCGAGGACAACGACGGTGGGTTGGT |
| 15 | DRB1-1316 | CTGAGAGAACGT | AGTTCGAGGACAACGACGGTGGGTTGAT |
| | DRB1-130201 | CTGAGAGAACGT | AGTTCGAGGACAACGACGGTGGGTTGCT |
| | DRB1-130202 | CTGAGAGAACGT | AGTTCGAGGACAACGACGGTGGGTTGCT |
| | DRB1-1331 | CTGAGAGAACGT | AGTTCGAGGACAACGACGGTGGGTTGGT |
| | DRB1-1339 | CTGAGAGAACGT | AGTTCGAGGACAACGACGGTGGGTTGGT |
| | DRB1-1341 | CTGAGAGAACGT | AGTTCGAGGACAACGACGGTGGGTTGGT |
| | DRB1-1309 | CTGAGAGAACGT | AGTTCGAGGACAAGGCGGGTGGGTTGTG |
| 20 | DRB1-1306 | CTGAGAGAACGT | AGTTCGAGGACAACGACGGTGGGTTGTG |
| | DRB1-1356 | CTGAGAGAACGT | AGTTCGAGGACCACAGCGGTGGGTTGGT |
| | DRB1-0311 | CTGAGAGAACGT | AGTTCGAGGACCAAGAAAGGTGGGTTGTG |
| | DRB1-0324 | CTGAGAGAACGT | AGTTCGAGGACCAAGAAAGGTGGGTTGTG |
| | DRB1-0320 | CTGAGAGAACGT | AGTTCGAGGACCAAGAAAGGGTGGGCTGTG |
| 25 | DRB1-030101 | CTGAGAGAACGT | AGTTCGAGGACCAAGAAAGGGTGGGTTGTG |
| | DRB1-030102 | CTGAGAGAACGT | AGTTCGAGGACCAAGAAAGGGTGGGTTGTG |
| | DRB1-0307 | CTGAGAGAACGT | AGTTCGAGGACCAAGAAAGGGTGGGTTGTG |
| | DRB1-0312 | CTGAGAGAACGT | AGTTCGAGGACCAAGAAAGGGTGGGTTGTG |
| | DRB1-0313 | CTGAGAGAACGT | AGTTCGAGGACCAAGAAAGGGTGGGTTGTG |
| | DRB1-0315 | CTGAGAGAACGT | AGTTCGAGGACCAAGAAAGGGTGGGTTGTG |
| | DRB1-0316 | CTGAGAGAACGT | AGTTCGAGGACCAAGAAAGGGTGGGTTGTG |
| | DRB1-0318 | CTGAGAGAACGT | AGTTCGAGGACCAAGAAAGGGTGGGTTGTG |
| | DRB1-0322 | CTGAGAGAACGT | AGTTCGAGGACCAAGAAAGGGTGGGTTGTG |
| | DRB1-0323 | CTGAGAGAACGT | AGTTCGAGGACCAAGAAAGGGTGGGTTGTG |
| 30 | DRB1-030501 | CTGAGAGAACGT | AGTTCGAGGACCAAGAAAGGGTGGGTTGGT |
| | DRB1-030502 | CTGAGAGAACGT | AGTTCGAGGACCAAGAAAGGGTGGGTTGGT |
| | DRB1-0309 | CTGAGAGAACGT | AGTTCGAGGACCAAGAAAGGGTGGGTTGGT |
| | DRB1-0314 | CTGAGAGAACGT | AGTTCGAGGACCAAGAAAGGGTGGGTTGGT |
| | DRB1-1421 | CTGAGAGAACGT | AGTTCGAGGACCAAGAAAGGGTGGGTTGTG |

| | | | | |
|----|-------------|--------------|-------|---------------------------|
| | DRB1-1417 | CTGAGAGAACGT | AGTT | CGAGGGACCAGAGCGGTGGGTTGTG |
| | DRB1-1430 | CTGAGAGAACGT | AGTT | CGAGGGACCAGAGCGGTGGGTTGGT |
| | DRB1-1433 | CTGAGAGAACGT | AGTT | CGAGGGACCAGAGAGGTGGGTTGTG |
| | DRB1-1320 | CTGAGAGAACGT | AGTT | CGAGGGACCACGACGGTGGGTTGTG |
| 5 | DRB1-1329 | CTGAGAGAACGT | AGTT | CGAGGGACCACGACGGTGGGTTGGT |
| | DRB1-1342 | CTGAGAGAACGT | AGTT | CGAGGGACTACAGCGGTGGGTTGTG |
| | DRB1-1305 | CTGAGAGAACGT | AGTT | CGAGGGACTACAGCGGTGGGTTGGT |
| | DRB1-1350 | CTGAGAGAACGT | AGTT | CGAGGGACTACAGCGGTGGGTTGGT |
| | DRB1-1318 | CTGAGAGAACGT | AGTT | CGAGGGACTACAGTGGTGGGTTGTG |
| 10 | DRB1-1116 | CTGAGAGAACGT | AGTT | GGAGGGACACGACGGTGGGTTGTG |
| | DRB1-1120 | CTGAGAGAACGT | AGTT | GGAGGGACACGACGGTGGGTTGGT |
| | DRB1-0308 | CTGAGAGAACGT | AGTT | GGAGGGACCAGAAGGGTGGGTTGTG |
| | DRB1-0310 | CTGAGAGAACGT | AGTT | GGAGGGACCAGAAGGGTGGGTTGTG |
| | DRB1-1343 | CTGAGAGAACGT | AGTT | GGAGGGACACGACGGTGGGTTGTG |
| | DRB1-1109 | CTGAGAGAACGT | AGTT | GGAGGGACTACAGCGGTGGGTTGGT |
| | DRB1-1128 | CTGAGAGAACGT | AGTT | GGAGGGACTACAGCGGTGGGTTGGT |
| 15 | DRB1-1140 | CTGAGAGAACGT | AGTT | GGAGGGACTACAGCGGTGGGTTGTG |
| | DRB1-1115 | CTGAGAGGACTT | AGTT | GGAGGGACTACAGCGGTGGGTTGGT |
| | DRB1-1124 | CTGAGAGGACGT | AGTT | GGAGGGACTACAGCGGTGGGTTGG |
| | DRB1-1362 | CTGAGAGGACTT | AGTT | CGAGGGACTACAGCGGTGGGTTGGT |
| | DRB1-1144 | CTGAGAGTACGC | AGTT | GGAGGGACTACAGCGGTGGGTTGTG |
| 20 | DRB1-130301 | CTGAGAGTACGT | AGTAC | CGAGGGACACAAAGGGTGGGTTGG |
| | DRB1-130302 | CTGAGAGTACGT | AGTAC | GGAGGGACACAAAGGGTGGGTTGG |
| | DRB1-1333 | CTGAGAGTACGT | AGTAC | GGAGGGACACAAAGGGTGGGTTGG |
| | DRB1-1337 | CTGAGAGTACGT | AGTAC | GGAGGGACACAAACGGTGGGTTGG |
| | DRB1-1338 | CTGAGAGTACGT | AGTAC | GGAGGGACACGACGGTGGGTTGG |
| | DRB1-1312 | CTGAGAGTACGT | AGTAC | GGAGGGACACAGCGGTGGGTTGG |
| | DRB1-1313 | CTGAGAGTACGT | AGTAC | GGAGGGACACAGTGGTGGGTTGGT |
| 25 | DRB1-1348 | CTGAGAGTACGT | AGTAC | GGAGGGACACGACGGTGGGTTGTG |
| | DRB1-1358 | CTGAGAGTACGT | AGTAC | GGAGGGACACAGCGGTGGGCTGTG |
| | DRB1-0317 | CTGAGAGTACGT | AGTAC | GGAGGGACAGAAAGGTGGGTTGG |
| | DRB1-0434 | CTGAGAGTACGT | AGTAC | GGAGGGACAGAACGGTGGGTTGGT |
| | DRB1-0820 | CTGAGAGTACGT | AGTAC | GGAGGGACTACAGTGGTGGGTTGTG |
| 30 | DRB1-130701 | CTGAGAGTACGT | AGTAC | GGAGGGACTACAGCGGTGGGTTGGT |
| | DRB1-1349 | CTGAGAGTACGT | AGTAC | GGAGGGACTACAGCGGTGGGTTGGT |
| | DRB1-1347 | CTGAGAGTACGT | AGTAC | GGAGGGACTACAGTGGTGGGTTGGT |
| | DRB1-1355 | CTGAGAGTACGT | AGTAC | GGAGGGACTACAGTGGTGGGTTGGT |

| | | |
|----|-------------|--|
| | DRB1-1141 | CTGAGAGTACGTAGTAGGAGGACTACGACGGTGGTTTGTG |
| | DRB1-1137 | CTGAGAGTACGTAGTAGGAGGACTACGACGGTGGTTTGTG |
| | DRB1-1425 | CTGAGAGTACGTAGTAGGAGGACTACGACGGTGGTTTGTG |
| | DRB1-130702 | CTGAGAGTACGTAGTATGAGGACTACGACGGTGGTTTGTG |
| 5 | DRB1-1442 | CTGAGAGTACGTAGTTCGAGGACCGGAGAGGTGGTTTGTG |
| | DRB1-1304 | CTGAGAGTACGTAGTTCGAGGACACGACGGTGGTTTGTG |
| | DRB1-1322 | CTGAGAGTACGTAGTTCGAGGACACGACGGTGGTTTGTG |
| | DRB1-1352 | CTGAGAGTACGTAGTTCGAGGACACGACGGTGGTTTGTG |
| | DRB1-1323 | CTGAGAGTACGTAGTTCGAGGACACGACGGTGGTTTGTG |
| | DRB1-1324 | CTGAGAGTACGTAGTTCGAGGACTACGACGGTGGTTTGTG |
| | DRB1-1354 | CTGAGAGTACGTAGTTCGAGGACTACGACGGTGGTTTGTG |
| 10 | DRB1-1311 | CTGAGAGTACGTAGTTCGAGGACACGACGGTGGTTTGTG |
| | DRB1-1330 | CTGAGAGTACGTAGTTCGAGGACACAGCGGTGGTTTGTG |
| | DRB1-1325 | CTGAGAGTACGTAGTTCGAGGACACAGCGGTGGTTTGTG |
| | DRB1-131401 | CTGAGAGTACGTAGTTCGAGGACACAGCGGTGGTTTGTG |
| | DRB1-1321 | CTGAGAGTACGTAGTTCGAGGACTACAGCGGTGGTTTGTG |
| | DRB1-1346 | CTGAGAGTACGTAGTTCGAGGACTACAGCGGTGGTTTGTG |
| 15 | DRB1-1344 | CTGAGAGTACGTAGTTCGAGGACAGACGGTGGTTTGTG |
| | DRB1-0325 | CTGAGAGTACGTAGTTCGAGGACAGAAGGGTGGTTTGTG |
| | DRB1-1102 | CTGAGAGTACGTAGTTGGAGGACACGACGGTGGTTTGTG |
| | DRB1-1121 | CTGAGAGTACGTAGTTGGAGGACACGACGGTGGCTGTG |
| | DRB1-1118 | CTGAGAGTACGTAGTTGGAGGACACAGCGGTGGTTTGTG |
| 20 | DRB1-1114 | CTGAGAGTACGTAGTTGGAGGACACGACGGTGGTTTGTG |
| | DRB1-1345 | CTGAGAGTACGTAGTTGGAGGACACGACGGTGGTTTGTG |
| | DRB1-1119 | CTGAGAGTACGTAGTTGGAGGACACAGCGGTGGTTTGTG |
| | DRB1-1131 | CTGAGAGTACGTAGTTGGAGGACACAGCGGTGGTTTGTG |
| | DRB1-1145 | CTGAGAGTACGTAGTTGGAGGACACAGTGGTGGTTTGTG |
| | DRB1-1136 | CTGAGAGTACGTAGTTGGAGGACACGACGGTGGTTTGTG |
| 25 | DRB1-1107 | CTGAGAGTACGTAGTTGGAGGACACAGGGTGGTTTGTG |
| | DRB1-1142 | CTGAGAGTACGTAGTTGGAGGACACAGCGGTGGTTTGTG |
| | DRB1-1134 | CTGAGAGTACGTAGTTGGAGGACACAGCGGTGGTTTGTG |
| | DRB1-110801 | CTGAGAGTACGTAGTTGGAGGACACAGCGGTGGTTTGTG |
| | DRB1-110802 | CTGAGAGTACGTAGTTGGAGGACACAGCGGTGGTTTGTG |
| | DRB1-1126 | CTGAGAGTACGTAGTTGGAGGACACAGCGGTGGTTTGTG |
| 30 | DRB1-1103 | CTGAGAGTACGTAGTTGGAGGACTACGACGGTGGTTTGTG |
| | DRB1-110601 | CTGAGAGTACGTAGTTGGAGGACTACAGCGGTGGCTGTG |
| | DRB1-110602 | CTGAGAGTACGTAGTTGGAGGACTACAGCGGTGGCTGTG |

| | |
|----------------|--|
| DRB1-1135 | CTGAGAGTACGTAGTTGGACGACTACAGCGGTGGGTTGTG |
| DRB1-110401 | CTGAGAGTACGTAGTTGGAGGACTACAGCGGTGGGTTGTG |
| DRB1-110402 | CTGAGAGTACGTAGTTGGAGGACTACAGCGGTGGGTTGTG |
| DRB1-1143 | CTGAGAGTACGTAGTTGGAGGACTACAGCGGTGGGTTGTG |
| DRB1-1146 | CTGAGAGTACGTAGTTGGAGGACTACAGCGGTGGGTTGTG |
| DRB1-1138 | CTGAGAGTACGTAGTTGGGGACTACAGCGGTGGGTTGTG |
| 5 DRB1-1125 | CTGAGAGTACGTAGTTGGAGGACTACAGCGGTGGGTTGTG |
| DRB1-1111 | CTGAGAGTACGTAGTTGGAGGACTACGACGGTGGGTTGGT |
| DRB1-1133 | CTGAGAGTACGTAGTTGGACGACTACAGCGGTGGGTTGGT |
| DRB1-110101 | CTGAGAGTACGTAGTTGGAGGACTACAGCGGTGGGTTGGT |
| DRB1-110102 | CTGAGAGTACGTAGTTGGAGGACTACAGCGGTGGGTTGTG |
| DRB1-110103 | CTGAGAGTACGTAGTTGGAGGACTACAGCGGTGGGTTGGT |
| DRB1-110104 | CTGAGAGTACGTAGTTGGAGGACTACAGCGGTGGGTTGTG |
| 10 DRB1-110105 | CTGAGAGTACGTAGTTGGAGGACTACAGCGGTGGGTTGTG |
| DRB1-112701 | CTGAGAGTACGTAGTTGGAGGACTACAGCGGTGGGTTGGT |
| DRB1-112702 | CTGAGAGTACGTAGTTGGAGGACTACAGCGGTGGGTTGGT |
| DRB1-1130 | CTGAGAGTACGTAGTTGGAGGACTACAGCGGTGGGTTGGT |
| DRB1-1139 | CTGAGAGTACGTAGTTGGAGGACTACAGCGGTGGGTTGGT |
| DRB1-1123 | CTGAGAGTACGTAGTTGGAGGACTACAGCGGTGGGTTGGT |
| DRB1-1132 | CTGAGAGTACGTAGTTGGAGGACTACAGCGGTGGGTTGGT |
| 15 DRB1-131402 | CTGAGAGTACGTAGTTGGAGGACTACAGCGGTGGGTTGGT |
| DRB1-0304 | CTGAGAGTCCGTAGTTGAGGACAGAAGGGTGGGTTGTG |
| DRB1-1129 | CTGAGAGTCCGTAGTTGGAGGACTACAGCGGTGGGTTGGT |
| DRB1-1147 | CTGAGAGTCCGTAGTTGGAGGACTACAGCGGTGGGTTGTG |
| DRB1-1360 | CTGAGAGTCCGTAGTATGAGGACACAGCGGTGGGTTGGT |
| 20 DRB1-1441 | CTGAGAGTCCTAGTACGAGGACAGAGCGGTGGGTTGGT |
| DRB1-1308 | CTGAGAGTCCGTAGTACGAGGACACGACGGTGGGTTGTG |
| DRB1-1319 | CTGAGAGTCCGTAGTACGAGGACACGACGGTGGGTTGTG |
| DRB1-140502 | CTGAGAGTCCGTAGTACGAGGACGGAGAGGTGGGTTGTG |
| DRB1-1423 | CTGAGAGTCCGTAGTACGAGGACGGAGAGGTGGGTTGTG |
| DRB1-1420 | CTGAGAGTCCGTAGTACGAGGACAGAGCGGTGGGTTGTG |
| 25 DRB1-1357 | CTGAGAGTCCGTAGTTGAGGACACGACGGTGGGTTGTG |
| DRB1-0321 | CTGAGAGTCCGTAGTTGAGGACAGAAGGGTGGGTTGTG |
| DRB1-1416 | CTGAGAGTCCGTAGTACGAGGACACGACGGTGGGTTGTG |
| DRB1-1117 | CTGAGAGTCCGTAGTACGAGGACGGAGAGGTGGGTTGTG |
| DRB1-140101 | CTGAGAGTCCGTAGTACGAGGACGGAGAGGTGGGTTGTG |
| DRB1-140102 | CTGAGAGTCCGTAGTACGAGGACGGAGAGGTGGGTTGTG |
| DRB1-1408 | CTGAGAGTCCGTAGTACGAGGACGGAGAGGTGGGTTGTG |
| DRB1-1426 | CTGAGAGTCCGTAGTACGAGGACGGAGAGGTGGGTTGTG |
| 30 DRB1-1438 | CTGAGAGTCCGTAGTACGAGGACGGAGAGGTGGGTTGTG |
| DRB1-1439 | CTGAGAGTCCGTAGTACGAGGACGGAGAGGTGGGTTGTG |
| DRB1-1432 | CTGAGAGTCCGTAGTACGAGGACGGAGAGGTGGGTTGTG |
| DRB1-1434 | CTGAGAGTCCGTAGTACGAGGACGGAGAGGTGGGTTGTG |

| | | |
|----|-------------|--|
| | DRB1-1113 | CTGAGAGTTTCGTAGTTGGAGGACCGGAGCGGTTGGTTGTG |
| | DRB1-1435 | CTGAGAGTTTCGTAGTTGGAGGACCGGAGAGGTTGGTTGTG |
| | DRB1-1437 | CTGAGAGTTTCGTAGTATGAGGACAAAGGCCGGTTGGTTGTG |
| | DRB1-1445 | CTGAGAGTTTCGTAGTATGAGGACAGGAGAGGTTGGTTGTG |
| 5 | DRB1-140501 | CTGAGAGTTTCGTAGTATGAGGACCGGAGAGGTTGGTTGTG |
| | DRB1-1443 | CTGAGAGTTTCGTAGTATGAGGACCGGAGAGGTTGGTTGTG |
| | DRB1-1110 | CTGAGAGTTTCGTAGTTGGAGGACTACAGCGGTTGGTTGGT |
| | DRB1-111201 | CTGAGAGTTTCGTAGTTGGAGGACTACAGCGGTTGGTTGGT |
| | DRB1-111202 | CTGAGAGTTTCGTAGTTGGAGGACTACAGCGGTTGGTTGGT |
| | DRB1-1414 | CTGAGAGTTTCGTAGTACGAGGACCGGAGAGGTTGGTTGGT |
| | DRB1-1436 | CTGAGAGTTTCGTAGTACGAGGACCGGAGAGGTTGGTTGGT |
| 10 | DRB1-140701 | CTGAGAGTTTCGTAGTACGGAGGACCGGAGAGGTTGGTTGGT |
| | DRB1-140702 | CTGAGAGTTTCGTAGTACGGAGGACCGGAGAGGTTGGTTGGT |
| | DRB1-1422 | CTGAGAGTTTCGTAGTACGGAGGACTACAGCGGTTGGTTGGT |
| | DRB1-1440 | CTGAGAGTTTCGTAGTACGAGGACACAGTGGTTGGTTGGT |
| | DRB1-1444 | CTGAGAGTTTCGTAGTATGAGGACCGGAGAGGTTGGTTGGT |
| 15 | DRB1-120101 | GTGAGAGCTCCTAGTTCGAGGACAAACAGCGGTTGGCTGTG |
| | DRB1-120102 | GTGAGAGCTCCTAGTTCGAGGACAAACAGCGGTTGGCTGTG |
| | DRB1-1206 | GTGAGAGCTCCTAGTTCGAGGACAAACAGCGGTTGGCTGTG |
| | DRB1-1207 | GTGAGAGCTCCTAGTTCGAGGACAAACAGCGGTTGGCTGTG |
| | DRB1-1208 | GTGAGAGCTCCTAGTTCGAGGACAAACAGCGGTTGGCTGTG |
| | DRB1-1209 | GTGAGAGCTCCTAGTTCGAGGACAAACAGCGGTTGGCTGTG |
| | DRB1-120302 | GTGAGAGCTCCTAGTTCGAGGACAAACAGCGGTTGGCTGTG |
| | DRB1-1204 | GTGAGAGCTCCTAGTTGGAGGACAAACAGCGGTTGGCTGTG |
| 20 | DRB1-120201 | GTGAGAGCTCCTAGTTCGAGGACTACAGCGGTTGGCTGTG |
| | DRB1-120202 | GTGAGAGCTCCTAGTTCGAGGACTACAGCGGTTGGCTGTG |
| | DRB1-0816 | GTGAGAGGACGTAGTACGAGGACTACAGTGGTTGGTTGGT |
| | DRB1-0818 | GTGAGAGTACGTAGTACGAGGACAAACAGCGGTTGGTTGGT |
| | DRB1-0825 | GTGAGAGTACGTAGTACGAGGACAAACAGCGGTTGGTTGGT |
| | DRB1-0810 | GTGAGAGTACGTAGTACGAGGACAAACAGTGGTTGGTTGGT |
| | DRB1-0812 | GTGAGAGTACGTAGTACGAGGACAAACAGTGGTTGGCTGTG |
| 25 | DRB1-080302 | GTGAGAGTACGTAGTACGAGGACAAACAGTGGTTGGTTGGT |
| | DRB1-0814 | GTGAGAGTACGTAGTACGAGGACAAACAGTGGTTGGTTGGT |
| | DRB1-0819 | GTGAGAGTACGTAGTACGAGGACAAACAGTGGTTGGTTGGT |
| | DRB1-0823 | GTGAGAGTACGTAGTACGAGGACAAACAGTGGTTGGTTGGT |
| | DRB1-0813 | GTGAGAGTACGTAGTACGAGGACAAACAGTGGTTGGTTGGT |
| | DRB1-080401 | GTGAGAGTACGTAGTACGAGGACTACAGTGGTTGGTTGTG |
| | DRB1-080404 | GTGAGAGTACGTAGTACGAGGACTACAGTGGTTGGTTGTG |
| | DRB1-0806 | GTGAGAGTACGTAGTACGAGGACTACAGTGGTTGGTTGTG |
| 30 | DRB1-0822 | GTGAGAGTACGTAGTACGAGGACTACAGTGGTTGGCTGTG |
| | DRB1-0805 | GTGAGAGTACGTAGTACGAGGACTACAGCGGTTGGTTGGT |
| | DRB1-0824 | GTGAGAGTACGTAGTACGAGGACTACAGCGGTTGGTTGGT |

| | | | | | | | | | | | | | | | | | | | | | | | | | |
|----|--|-------------|----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|----|----|----|----|----|-----|
| | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | DRB1-080101 | GT | G | A | G | A | G | T | A | C | G | A | G | G | A | C | A | G | T | GG | T | GG | T | GG |
| | | DRB1-080102 | GT | G | A | G | A | G | T | A | C | G | A | G | G | A | C | A | G | T | GG | T | GG | T | GG |
| | | DRB1-080201 | GT | G | A | G | A | G | T | A | C | G | A | G | G | A | C | A | G | T | GG | T | GG | T | GG |
| | | DRB1-080202 | GT | G | A | G | A | G | T | A | C | G | A | G | G | A | C | A | G | T | GG | T | GG | T | GG |
| | | DRB1-080203 | GT | G | A | G | A | G | T | A | C | G | A | G | G | A | C | A | G | T | GG | T | GG | T | GG |
| | | DRB1-0807 | GT | G | A | G | A | G | T | A | C | G | A | G | G | A | C | A | G | T | GG | T | GG | T | GG |
| | | DRB1-0811 | GT | G | A | G | A | G | T | A | C | G | A | G | G | A | C | A | G | T | GG | T | GG | T | GG |
| 5 | | DRB1-080402 | GT | G | A | G | A | G | T | A | C | G | A | G | G | A | C | A | G | T | GG | T | GG | T | GG |
| | | DRB1-080403 | GT | G | A | G | A | G | T | A | C | G | A | G | G | A | C | A | G | T | GG | T | GG | T | GG |
| | | DRB1-0808 | GT | G | A | G | A | G | T | A | C | G | A | G | G | A | C | A | G | T | GG | T | GG | T | GG |
| | | DRB1-0815 | GT | G | A | G | A | G | T | A | C | G | A | G | G | A | C | A | G | T | GG | T | GG | T | GG |
| | | DRB1-0817 | GT | G | A | G | A | G | T | A | C | G | A | G | G | A | C | A | G | T | GG | T | GG | T | GG |
| 10 | | DRB1-1317 | GT | G | A | G | A | G | T | A | C | G | A | G | G | A | C | A | G | T | GG | T | GG | T | GG |
| | | DRB1-1105 | GT | G | A | G | A | G | T | A | C | G | A | G | G | A | C | A | G | C | GG | T | GG | T | GG |
| | | DRB1-0809 | GT | G | A | G | A | G | T | A | C | G | A | G | G | A | C | A | G | T | GG | T | GG | T | GG |
| | | DRB1-0821 | GT | G | A | G | A | G | T | A | C | G | A | G | G | A | C | A | G | T | GG | T | GG | T | GG |
| | | DRB1-1415 | GT | G | A | G | A | G | T | C | G | A | G | G | A | C | A | G | T | GG | T | GG | T | GG | |
| | | DRB1-1205 | GT | G | A | G | A | G | T | C | C | T | A | G | G | A | C | A | G | C | GG | T | GG | C | T |
| 15 | | DRB1-1404 | GT | G | A | G | A | G | T | C | G | T | A | G | G | A | C | A | G | T | GG | T | GG | T | TGT |
| | | DRB1-1411 | GT | G | A | G | A | G | T | C | G | T | A | G | G | A | C | A | G | T | GG | T | GG | T | TGT |
| | | DRB1-1428 | GT | G | A | G | A | G | T | C | G | T | A | G | G | A | C | A | G | T | GG | T | GG | C | TGT |
| | | DRB1-1431 | GT | G | A | G | A | G | T | C | G | T | A | G | G | A | C | A | G | T | GG | T | GG | T | TGT |
| | | DRB1-1507 | GG | G | A | G | A | G | T | C | C | T | A | G | G | A | C | A | G | G | GG | T | GG | T | TGT |
| 20 | | DRB1-1511 | GG | G | A | G | A | G | T | C | C | T | A | G | G | A | C | A | G | G | GG | T | GG | T | GG |
| | | DRB1-1605 | GG | G | A | G | A | G | T | C | C | T | A | G | G | A | C | A | G | C | GG | T | GG | T | GG |
| | | DRB1-1607 | GG | G | A | G | A | G | T | C | C | T | A | G | G | A | C | A | G | C | GG | T | GG | T | GG |
| | | DRB1-160201 | GG | G | A | G | A | G | T | C | C | T | A | G | G | A | C | A | G | C | GG | T | GG | T | GG |
| | | DRB1-160202 | GG | G | A | G | A | G | T | C | C | T | A | G | G | A | C | A | G | C | GG | T | GG | T | GG |
| | | DRB1-160101 | GG | G | A | G | A | G | T | C | C | T | A | G | G | A | C | A | G | C | GG | T | GG | T | GG |
| | | DRB1-160102 | GG | G | A | G | A | G | T | C | C | T | A | G | G | A | C | A | G | C | GG | T | GG | T | GG |
| | | DRB1-160103 | GG | G | A | G | A | G | T | C | C | T | A | G | G | A | C | A | G | C | GG | T | GG | T | GG |
| 25 | | DRB1-1604 | GG | G | A | G | A | G | T | C | C | T | A | G | G | A | C | A | G | T | GG | T | GG | T | GG |
| | | DRB1-150104 | GG | G | A | G | A | G | T | C | C | T | A | G | G | A | C | A | G | G | GG | T | GG | T | TGT |
| | | DRB1-1512 | GG | G | A | G | A | G | T | C | C | T | A | G | G | A | C | A | G | G | GG | T | GG | T | TGT |
| | | DRB1-150202 | GG | G | A | G | A | G | T | C | C | T | A | G | G | A | C | A | G | G | GG | T | GG | T | GG |
| | | DRB1-1510 | GG | G | A | G | A | G | T | C | C | T | A | G | G | A | C | A | G | C | GG | T | GG | T | TGT |
| 30 | | DRB1-1508 | GG | G | A | G | A | G | T | C | C | T | A | G | G | A | C | A | G | A | GG | C | GG | T | GG |
| | | DRB1-150102 | GG | G | A | G | A | G | T | C | C | T | A | G | G | A | C | A | G | C | GG | T | GG | T | TGT |
| | | DRB1-150101 | GG | G | A | G | A | G | T | C | C | T | A | G | G | A | C | A | G | C | GG | T | GG | T | TGT |
| | | DRB1-150103 | GG | G | A | G | A | G | T | C | C | T | A | G | G | A | C | A | G | C | GG | T | GG | T | TGT |

| | | | | | | |
|----|-------------|--------------|-------|-----------|----------|----------|
| | DRB1-150105 | GGGAGAGTCCGT | AGTT | TGAGGGACA | AGGCCGGT | GGGTTGTG |
| | DRB1-1503 | GGGAGAGTCCGT | AGTT | TGAGGGACA | AGGCCGGT | GGGTTGTG |
| | DRB1-1506 | GGGAGAGTCCGT | AGTT | TGAGGGACA | AGGCCGGT | GGGTTGTG |
| | DRB1-1509 | GGGAGAGTCCGT | AGTT | TGAGGGACA | AGGCCGGT | GGGTTGTG |
| | DRB1-1513 | GGGAGAGTCCGT | AGTT | TGAGGGACA | AGGCCGGT | GGGTTGTG |
| 5 | DRB1-150201 | GGGAGAGTCCGT | AGTT | TGAGGGACA | AGGCCGGT | GGGTTGTG |
| | DRB1-150203 | GGGAGAGTCCGT | AGTT | TGAGGGACA | AGGCCGGT | GGGTTGTG |
| | DRB1-1505 | GGGAGAGTCCGT | AGTT | TGAGGGACC | AGGCCGGT | GGGTTGTG |
| | DRB1-1504 | GGGAGAGTCCGT | AGTT | TGAGGGACT | AGGCCGGT | GGGTTGTG |
| | DRB1-1608 | GGGAGAGAACGT | AGTAT | TGAGGGACT | ACAGCGGT | GGGTTGGT |
| | DRB1-090102 | TTGAGAGAACGT | AGTAC | CGAGGACT | GGAGAGG | GGGTTGGT |
| | DRB1-0902 | TTGAGAGAACGT | AGTAT | TGAGGACT | GGAGAGG | GGGTTGGT |
| 10 | DRB1-010102 | TTGAGAGAACGT | AGTAC | CGAGGACC | AGAGCGGT | GGGTTGGT |
| | DRB1-0108 | TTGAGAGAACGT | AGTAC | CGAGGACC | AGAGCGGT | GGGTTGGT |
| | DRB1-100101 | TTGAGAGAACGT | AGTAC | CGAGGACC | GGAGCGGT | GGGTTGGT |
| | DRB1-100102 | TTGAGAGAACGT | AGTAC | CGAGGACC | GGAGCGGT | GGGTTGGT |
| | DRB1-0103 | TTGAGAGTCCGT | AGTAC | CGAGGACA | ACGACGGT | GGGTTGGT |
| 15 | DRB1-0110 | TTGAGAGTCCGT | AGTAC | CGAGGACC | AGAACGGT | GGGTTGGT |
| | DRB1-0106 | TTGAGAGTCCGT | AGTAC | CGAGGACC | AGGCCGGT | GGGTTGTG |
| | DRB1-0109 | TTGAGAGTCCGT | AGTAC | CGAGGACC | AGGCCGGT | GGGTTGGT |
| | DRB1-010202 | TTGAGAGTCCGT | AGTAC | CGAGGACC | AGAGCGGT | GGGCTGTG |
| | DRB1-010201 | TTGAGAGTCCGT | AGTAC | CGAGGACC | AGAGCGGT | GGGCTGTG |
| | DRB1-0104 | TTGAGAGTCCGT | AGTAC | CGAGGACC | AGAGCGGT | GGGTTGTG |
| 20 | DRB1-010101 | TTGAGAGTCCGT | AGTAC | CGAGGACC | AGAGCGGT | GGGTTGGT |
| | DRB1-0105 | TTGAGAGTCCGT | AGTAC | CGAGGACC | AGAGCGGT | GGGTTGGT |
| | DRB1-0107 | TTGAGAGTCCGT | AGTAC | CGAGGACC | AGAGCGGT | GGGTTGGT |
| | DRB1-0111 | TTGAGAGTCCGT | AGTAC | CGAGGACC | AGAGCGGT | GGGTTGGT |

General strategy for medium resolution typing is described below:

For medium resolution typing a maximally informative set of marker positions were determined. These consist of positions 98, 414, 539, 282, 571, 368, 256, 292, 238, 270, 453, 527, 502, 81, 268, 559, 92, 123 and 396 of HLA-A (numbering starts at the transcription start position of exon 1), positions 539, 419, 559, 412, 272, 362, 302, 363, 206, 369, 259, 97, 583, 292, 222, 527, 418, 435 and 571 of HLA-B (numbering starts at the transcription start position of exon 1), and positions 125, 196, 197, 227, 261, 286, 299, 308, 341 and 345 of HLA-DRB1 (numbering starts at the transcription start position of exon 1).

10

In general, the order of the positions is from the most informative to the least informative with respect to the selection criteria of frequent and rare HLA alleles (see list of frequent HLA alleles above). Thus the ten markers (HLA-A and HLA-B) that were selected for the fine typing strategy constitute the first ten markers of the set of 19 markers for the single pass classification into frequent and rare HLA alleles (HLA-A and HLA-B). Like with sequence-based HLA typing there are heterozygous combinations of HLA alleles that can not be resolved. However, there are fewer ambiguities with this method due to the mini-haplotypes that are provided.

20

Another object of the present invention is the use of said methodology of the invention is for screening of tissue donors, for example, bone marrow donors in registries for frequent and rare HLA types.

25 The description of the HLA alleles is based on the Anthony Nolan database (www.ebi.ac.uk/imgt/hla/).

30 In addition to the aforementioned method, the invention includes yet other arrangements which will emerge from the description that follows, which refers to examples of supports according to the invention, as well as the annexed figures and tables, wherein:

Figure 1 describes 19 positions covered by mini-haplotyping assays for discrimination of HLA-A mapped onto the HLA-A allele A*010101 as reference. Black boxes indicate an extension position while grey boxes indicate polymorphisms that are captured by the annealing of the respective primer of the primer pool. Pools are used in forward and reverse. Numbering is according to the transcription start of the cDNA.

Figure 2 describes 19 positions covered by mini-haplotyping assays for discrimination of HLA-B mapped onto the HLA-B allele B*070201 as reference.

10 Black boxes indicate an extension position while grey boxes indicate polymorphisms that are captured by the annealing of the respective primer of the primer pool. Pools are used in forward and reverse. Numbering is according to the transcription start of the cDNA.

15 Figure 3 describes 10 positions covered by mini-haplotyping assays for discrimination of HLA-DRB1 mapped onto the HLA-DRB1 allele DRB1*0101 as reference. Black boxes indicate an extension position while grey boxes indicate polymorphisms that are captured by the annealing of the respective primer of the primer pool. Pools are used in forward and reverse. Numbering is according to the transcription start of the cDNA.

20

Figure 4 describes 10 positions covered by mini-haplotyping assays for discrimination of HLA-A mapped onto the HLA-A allele A*010101 as reference for the distinction of subgroups that can then be further analysed. Black boxes indicate an extension position while grey boxes indicate polymorphisms that are captured by the annealing of the respective primer of the primer pool. Pools are used in forward and reverse. Numbering is according to the transcription start of the cDNA.

30 Figure 5 describes 10 positions covered by mini-haplotyping assays for discrimination of HLA-B mapped onto the HLA-B allele B*070201 as reference for the distinction of subgroups that can then be further analysed. Black boxes indicate

an extension position while grey boxes indicate polymorphisms that are captured by the annealing of the respective primer of the primer pool. Pools are used in forward and reverse. Numbering is according to the transcription start of the cDNA.

5 Figure 6 shows genotyping results of a CEPH family (1418, 01 = father, 02 = mother, 03 = child, 04 = child) for position HLA-B_272. 1407,3 Da corresponds to the addition of C to primer 6, 7, 8, or 9; 1422,3 Da corresponds to the addition of T to primer 6, 7, 8, or 9; 1431,4 Da/ 1430,9 Da corresponds to the addition of A to primer 6, 7, 8, or 9; and 1447,4 Da/ 1448,5 Da corresponds to the addition of G to 10 primer 6, 7, 8, or 9.

Table I represents HLA-A alleles captured by the 10 markers in the different subgroups and additional positions that have to be typed to resolve the subgroups.

15 Table II represents HLA-B alleles captured by the 10 markers in the different subgroups and additional positions that have to be typed to resolve the subgroups.

Table III represents HLA-DRB1 alleles captured by the 10 markers in the different subgroups and additional positions that have to be typed to resolve the subgroups.

20

Table IV represents the list of the individual primers that are required to constitute the pools for mini-haplotyping of HLA-A (19 markers). The 10 markers required for the creation of subgroups are also contained. ^ refers to the base used to attach the mass/charge tag, CT refers to the mass difference of the mass/charge tag, sp 25 means phosphorothioate group. The product analysed by mass spectrometry means phosphorothioate group. The product analysed by mass spectrometry includes the base 5' of the most 5' phosphorothioate (sp).

Table V represents the list of the individual primers that are required to constitute the pools for mini-haplotyping of HLA-B (19 markers). The 10 markers required 30 for the creation of subgroups are also contained. ^ refers to the base used to attach the mass/charge tag, CT refers to the mass difference of the mass/charge tag, sp

means phosphorothioate group. The product analysed by mass spectrometry includes the base 5' of the most 5' sp.

Table VI represents the list of the individual primers that are required to constitute 5 the pools for mini-haplotyping of HLA-DRB1 (10 markers). ^ refers to the base used to attach the mass/charge tag, CT refers to the mass difference of the mass/charge tag, sp means phosphorothioate group. The product analysed by mass spectrometry includes the base 5' of the most 5' sp.

10 Table VII represents the resolution that can be generated with the 19 markers for the distinction of the frequent HLA alleles in HLA-A.

Table VIII represents the resolution that can be generated with the 19 markers for the distinction of the frequent HLA alleles in HLA-B.

15 Table IX represents the resolution that can be generated with the 10 markers for the distinction of the frequent HLA alleles in HLA-DRB1.

Table X represents the list of HLA-A alleles that are resolved with the 10 markers 20 for the creation of subgroups. Each subgroup is separated by an empty line. Frequent alleles are shaded in darker grey, while lighter grey indicates the position that primers are extended onto.

Table XI represents the list of HLA-B alleles that are resolved with the 10 markers 25 for the creation of subgroups. Each subgroup is separated by an empty line. Frequent alleles are shaded in darker grey, while lighter grey indicates the position that primers are extended onto.

Table XII represents the list of HLA-DRB1 alleles that are resolved with the 10 markers 30 for the creation of subgroups. Each subgroup is separated by an empty line. Frequent alleles are shaded in darker grey, while lighter grey indicates the position that primers are extended onto.

Examples

Example 1: Mini-haplotyping at position 272 of HLA-B by the modified GOOD-
5 Assay

A locus specific PCR product of exon 2 and exon 3 of HLA-B is amplified with a set of primers published by the International Histocompatibility Working Group, Technical Manuals (Hurly, Fernandes-Vina, Gao, Middleton, Noreen, Ren and Smith; www.ihwg.org/tmanual/Tmcontents.htm). The PCR product is incubated with SAP to remove all excess dNTPs. Then a single base primer extension at position 272 in the PCR amplicon is carried out. The set of primers, to generate the mini-haplotypes is shown in Table V. Thereafter a 5'phosphodiesterase digest is applied to reduce the primers to a core sequence. After alkylation of the DNA 10 backbone of the mini-haplotype fragments the products are transferred onto a MALDI target pre-coated with matrix. Alternatively the matrix solution can be mixed with the samples and transferred onto the MALDI target to dry. The MALDI target is introduced into a MALDI mass spectrometer and analysed. The mass 15 spectra show one or two mass peaks and that correspond to specific mini-haplotypes.

15
20

PCR:

Forward primer, BAmp1 5'-G GGT CCC AGT TCT AAA GTC CCC ACG-
3' (1.875 pmol), reverse primer, BAmp2 5'-CC ATC CCC GGC GAC CTA TAG
25 GAG ATG-3' (1.875 pmol) an BAmp3 5'-AGG CCA TCC CGG CGG GCG ATC
TAT-3' (1.875 pmol), 0.25 μ l 10x PCR buffer (HiFi Platinum Taq)), 0.3 μ l MgSO₄
(50 mM), 0.2 μ l of a mix of each dCTP, dATP, dGTP and dTTP (2 mM each),
0.25U engineered DNA polymerase (HiFi Platinum DNA Polymerase; Invitrogen)
and 5 ng DNA fill to 3 μ l with water. Cycling: 1. 94°C 3 min, 2. 94°C 20 sec, 3.
30 64°C 30 sec, 4. 72°C 30 sec, steps 2 to 4 are repeated 35 times, 5. 72°C 5 min.

SAP digest:

1.75 μ l of 50 mM Tris-HCl and 0.25 μ l SAP (USB corporation, Cleveland, USA) are to add to the PCR product and this has to be incubated for 60 min at 37°C, followed by an incubation at 90°C for 10 min to denature the SAP enzyme.

5 Single Base Primer Extension:

To the SAP treated PCR product 2 μ l of an extension mix is to add. This mix contains 15 mM MgCl₂, 0.1 mM of each of the four α -S-ddNTPs, 5 pmol of the extension primers set and 0.4 U of Thermosequenase. Cycling: 1. 94°C 2 min, 2. 94°C 15 sec, 3. 58°C 20 sec, 4. 72°C 20 sec, steps 2 to 4 are repeated 50 times.

10

PDE digest:

To the extension product has to be added 0.5 μ l 0.5 M acetic acid and 1.5 μ l PDE (5.1U) and incubate for at lease 120 min at 37 °C.

15 Alkylation:

The alkylation is carried out by adding 21 μ l of an alkylation mix and incubate for 15 min at 40°C. Th alkylation mix contains 377 parts water free acetonitrile, 15 parts of 2M triethylamine/CO₂ (pH ~7.5), 75 parts 2mM Tris-HCl and 174 parts of methyliodine.

20 The alkylation is to stopped by adding 10 μ l deionised water. 5 μ l of the resulting upper phase are to dilute in 10 μ l 40% acetonitrile.

25 For MALDI target preparation and measurement with the MALDI mass spectrometer 0.5 μ l of the final dilution are transferred onto a MALDI target pre-coated with matrix (α -cyano-4-hydroxycinnamic acid methyl ester). Measurement was carried out in a Bruker Autoflex with typically -18 kV acceleration voltage, pulsed ion extraction with a delay of 200 ns, and detection in linear detection mode. Results for CEPH family 1418 are shown in figure 6.

30

Example 2: HLA-DR typing by the GOOD-Assay

A locus specific PCR for HLA-DRB is carried out. Therefore a set of allele-specific primers as listed below is used. These primers are published by J. Wu et al. in <http://www.ihwg.org/tmanual/TMcontents.htm> Chapter 10-B.

| Name | Sequence |
|-----------------|-----------------------------|
| Amp1_DRB1_f20 | 5'-TTCTTGTGGSAGCTTAAGTT-3' |
| Amp2_DRB1_f21 | 5'-TTCCTGTGGCAGCCTAAGAGG-3' |
| Amp3_DRB1_f22 | 5'-CACGTTCTGGAGTACTCTAB-3' |
| Amp3-2_DRB1_f23 | 5'-CGTTCTGGAGTACTCTACGGG-3' |
| Amp3-3_DRB1_f23 | 5'-CGTTCTGGAGTACTCTACGTC-3' |
| Amp4_DRB1_f21 | 5'-GTTTCTGGAGCAGGTTAAC-3' |
| DR7_DRB1_f20 | 5'-CCTGTGGCAGGGTAARTATA-3' |
| DR9_DRB1_f18 | 5'-CCCAACCACGTTCTTGA-3' |
| DR10_DRB1_f19 | 5'-AGACCACGTTCTGGAGG-3' |
| AmpB_DRB1_r18 | 5'-TCGCCGCTGCACYGTGAA-3' |

5

This set of primers carries a high risk of co-amplifying genes for the other HLA-DRB chains, which results in unclear results. However, this is currently the best available option for the PCR of HLA-DRB1. In order to resolve the problem an additional mini-haplotyping test can be added. The mini-haplotyping assay HLA-DRB_122-126 gives good resolution of HLA-DRB genes and allows the verification of results produced for typing of HLA-DRB1 PCR products. The identification of HLA-DRB1 genes is possible, as well as the identification of other amplified HLA-DRB genes which are present is possible. The set of primers listed below is used for the primer extension reaction. The details of the protocol are identical to example 1.

| Name | Sequence | CT | Masses | | | | |
|------------------|-----------------------------|-----|--------|--------|--------|--------|--------|
| | | | Primer | A | C | G | T |
| HLADR_1221_2f20 | TGAAGAAATGACACTCAspTspG*spT | 0 | 1487,5 | - | - | - | 1805,7 |
| HLADR_1222_2f20 | TGCAGAAATAGCACTCGspTspG*spT | 0 | 1503,5 | - | - | - | 1821,7 |
| HLADR_1223_2f20 | TGAAGAAATGACACTCAspGspG*spT | 0 | 1512,5 | - | - | - | 1830,7 |
| HLADR_1224_2f20 | TGAAGAAATGACACTTAspTspA*spT | 0 | 1471,5 | - | - | - | 1789,7 |
| HLADR_1225_2f20 | TGAAGAAATGACACTCCspCspT*spC | -14 | 1510,6 | - | - | - | 1814,8 |
| HLADR_1226_2f20 | TGAAGAAATRACACTCAspCspC*spC | -28 | 1418,4 | 1717,7 | 1693,6 | 1733,7 | - |
| HLADR_1227_2f20 | TGAAGAAATGACACTCAspTspA*spC | -14 | 1456,5 | - | - | - | 1760,7 |
| HLADR_1228_2f20 | TGAAGAAWTGACACTCAspGspA*spC | 0 | 1481,5 | - | - | - | 1799,7 |
| HLADR_1229_2f20 | TGAGGAAATGACACTCAspCspA*spC | -14 | 1441,5 | - | - | 1770,8 | 1745,7 |
| HLADR_12210_2f20 | TGAAGATATGACACTCAspCspA*spC | -14 | 1441,5 | - | - | 1770,8 | 1745,7 |
| HLADR_12211_2f20 | TGAAGAAATGACAYTCAspAspA*spC | 0 | 1465,5 | - | - | - | 1783,7 |

Of the thirteen possible mini-haplotypes, four represent genes other than HLA-DRB1. The mini-haplotype GTGTT (1821.7 Da), AACAC in sense direction, represents with 100% certainty co-amplification of the HLA-DRB9 gene. The mini-haplotype ATACT (1760.8 Da), AGTAT in sense direction, represent either all 5 HLA-DRB1*07 alleles (except HLA-DRB1*070102) or co-amplification of the HLA-DRB5 gene. The type TGTGT (1745.7 Da), AGTGT in sense direction, correspond to co-amplification or all variations of the HLA-DRB4 or HLA-DRB6 genes. Finally the type AGACT (1799.7 Da), AGTCT in sense direction, represent besides HLA-DRB1*1130 and HLA-DRB1*1446 also co-amplification of all 10 variants of HLA-DRB3 and HLA-DRB7 genes.